

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 19:33:26 ; Search time 51 Seconds
(without alignments)
989.707 Million cell updates/sec

Title: US-10-024-806-2

Perfect score: 1560

Sequence: 1 MATAAATAAAVSSPAARG.....NPAASYMTGQVLTDGGVMV 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1093	70.1	315	17 AAR89323	Rape leaf beta-ket
2	1093	70.1	315	17 AAR89322	Rape seed beta-ket
3	984	63.1	308	21 AAG35504	Arabidopsis thalia
4	981.5	62.9	267	21 AAG35505	Arabidopsis thalia
5	838	53.7	273	21 AAG40275	Arabidopsis thalia
6	835.5	53.6	232	21 AAG40276	Arabidopsis thalia
7	717.5	46.0	248	21 AAY54422	Amino acid sequenc
8	686.5	44.0	247	23 ABB48892	Listeria monocytog
9	676.5	43.4	165	21 AAG35506	Arabidopsis thalia

10	661.5	42.4	244	24 ABU18966	Pathogen specific
11	658.5	42.2	246	21 AAB15707	Staphylococcus aur
12	658.5	42.2	246	22 AAU33965	Staphylococcus aur
13	658.5	42.2	246	22 AAU36530	Staphylococcus aur
14	658.5	42.2	246	22 AAU37210	Staphylococcus aur
15	658.5	42.2	246	22 AAU37507	Staphylococcus aur
16	658.5	42.2	246	22 AAE02195	S. aureus NADPH-de
17	647.5	41.5	249	23 ABP39980	Staphylococcus epi
18	612.5	39.3	243	23 ABB54087	Lactococcus lactis
19	598.5	38.4	245	22 AAU35328	Enterococcus faeca
20	597.5	38.3	243	19 AAW80670	S. pneumoniae fatt
21	597.5	38.3	243	21 AAB15706	Streptococcus pneu
22	597.5	38.3	243	22 AAU37767	Streptococcus pneu
23	597.5	38.3	243	22 AAU37988	Streptococcus pneu
24	596.5	38.2	243	22 AAW01032	CFE 35 protein seq
25	596.5	38.2	243	24 ABU00775	S. pneumoniae type
26	587.5	37.7	243	23 ABP27345	Streptococcus poly
27	580.5	37.2	244	23 ABP28011	Streptococcus poly
28	576.5	37.0	244	21 AAY54421	Amino acid sequenc
29	576.5	37.0	244	22 AAU34533	E. coli cellular p
30	573.5	36.8	244	23 ABU10969	Poly3-hydroxybutan
31	573.5	36.8	244	23 AAG96548	Human short chain
32	556	35.6	247	21 AAB03794	3-ketoacyl-ACP red
33	556	35.6	247	22 AAU36300	Pseudomonas aerugi
34	555	35.6	282	24 ABP77406	N. gonorrhoeae ami
35	545.5	35.0	242	22 AAU35381	Haemophilus influe
36	530.5	34.0	248	20 AAY36959	Chlamydia trachoma
37	529	33.9	247	21 AAY95746	Bacillus megaterium
38	528	33.8	251	20 AAY34891	Chlamydia pneumonia
39	500.5	32.1	240	23 ABP27344	Streptococcus poly
40	499.5	32.0	171	22 AAG82281	S. epidermidis ope
41	496.5	31.8	247	20 AAW90010	Expressed antigen
42	496.5	31.8	247	22 AAU35749	Helicobacter pylor
43	488	31.3	248	20 AAW89908	Antigen 1 from clu
44	488	31.3	254	23 AAG31755	Protein with hydro
45	487.5	31.2	241	12 AAR10679	Acetoacetyl CoA re

ALIGNMENTS

RESULT 1

AAR89323

ID AAR89323 standard; Protein; 315 AA.

XX AAR89323;

AC AAR89323;

XX 13-APR-1996 (first entry)

XX Rape leaf beta-ketoacyl-ACP-ketoreductase.

XX Rape; leaf; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase;

XX plasmid pJR16.2; cDNA library; Escherichia coli; vector;

XX plasmid; stroma; transit peptide; cassette; antisense; oilseed;

XX transgenic plant; crop improvement; lipid; metabolic engineering;

XX polymer; rapeseed oil.

XX Brassica napus.

XX Key

XX Location/Qualifiers

XX Peptide

XX 1..55

XX /note= "transit peptide"

XX WO9602652-A2.

XX 01-FEB-1996.

XX 17-JUL-1995; 95WO-GB01678.

XX 20-JUL-1994; 94GB-0014622.

XX (ZENE) ZENECA LTD.

XX

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PI Chase D, Elborough K, Fentem PA, Slabas AR, White A;
XX WPI; 1996-105914/11.
DR N-PSDB; AAQ99305.
XX
XX New isolated rape beta-ketoreductase DNA - used to develop plants
PT with lower or higher oil contents or with altered oil compsn.
XX
XX Claim 2; Page 16; 29pp; English.
XX
XX The sequence corresponds to a rape leaf beta-ketoreductase encoded
CC by a cDNA insert in plasmid pJRS10.1 in Escherichia coli XL1-Blue.
CC A plastid stroma targeting transit peptide is present. DNA
CC encoding the protein may be inserted in a vector or expression
CC cassette in sense or antisense orientation for expression in an
CC oilseed plant, e.g. for production of transgenic rape plants with
CC low or modified oil content, diversion of metabolism to alternative
CC storage compounds, e.g. starch, protein or engineered polymers, or
CC production of plants with enhanced oil content. The DNA may also
CC be used as a probe to obtain similar genes from other plants. The
CC transit peptide may be used to direct other proteins to leaf
CC plastids.
XX
SQ Sequence 315 AA;
Query Match 70.1%; Score 1093; DB 17; Length 315;
Best Local Similarity 80.7%; Pred. No. 5.1e-80;
Matches 213; Conservative 28; Mismatches 23; Indels 0; Gaps 0;
Qy 55 VOTHVAVEQAVVKDATKLEAPVVTGASRGIGKATALGKAGCKVLVNYARSSKEAE 114
Db 52 VKAQTAVEQSTGEAVPKVESPVVVTGASRGIGKATALGKAGCKVLVNYARSSKEAE 111
Qy 115 EVSKEIASGGEAITFGGDSKEADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRMK 174
Db 112 EVSKEIASGGEAITFGGDSKEADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRMK 171
Qy 175 SQWODVIDLNLGTGVFLCTQATKVMKKRKKIINIASVGLTGNVGOANYSAKAGVIG 234
Db 172 SQWDEVIDLNLGTGVFLCTQATKVMKKRKKIINIASVGLTGNVGOANYSAKAGVIG 231
Qy 235 FTKTVAREYASRNINVAIAFGFIASDMTAELEKELKILSTIPLGRYGQPEEVAGLVE 294
Db 232 FSKTAAREGASRNINNVVCGFIASDMTAKLGEDMEKILGTIPLGRYGQPEEVAGLVE 291
Qy 295 FLALNPAASYMTGQVLTIDGGMMV 318
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RESULT 2
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ID AAR89322 standard; Protein; 315 AA.
XX
XX AAR89322;
XX
XX 13-APR-1996 (first entry)
XX
XX Rape seed beta-ketoacyl-ACP-ketoreductase.
XX
XX Rape, seed; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase;
KW plasmid pJRS10.1; cDNA library; embryo; Escherichia coli; vector;
KW plastid; stroma; transit peptide; cassette; antisense; oilseed;
KW transgenic plant; crop improvement; lipid; metabolic engineering;
KW polymer; rapeseed oil.
XX
XX Brassica napus.
XX
XX Key Location/Qualifiers
FH Peptide 1..56
FT /note= "transit peptide"
XX
XX WO9602652-A2.
^ PN
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XX
PD 01-FEB-1996.
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XX 17-JUL-1995; 95WO-GB01678.
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XX 20-JUL-1994; 94GB-0014622.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Chase D, Elborough K, Fentem PA, Slabas AR, White A;
XX WPI; 1996-105914/11.
DR N-PSDB; AAQ99304.
XX
XX New isolated rape beta-ketoreductase DNA - used to develop plants
PT with lower or higher oil contents or with altered oil compsn.
XX
XX Claim 1; Page 15; 29pp; English.
XX
XX The sequence corresponds to a rape seed beta-ketoreductase encoded
CC by a cDNA insert in plasmid pJRS10.1 in Escherichia coli XL1-Blue.
CC A plastid stroma targeting transit peptide is present. DNA
CC encoding the protein may be inserted in a vector or expression
CC cassette in sense or antisense orientation for expression in an
CC oilseed plant, e.g. for production of transgenic rape plants with
CC low or modified oil content, diversion of metabolism to alternative
CC storage compounds, e.g. starch, protein or engineered polymers, or
CC production of plants with enhanced oil content. The DNA may also
CC be used as a probe to obtain similar genes from other plants. The
CC transit peptide may be used to direct other proteins to seed
CC plastids.
XX
SQ Sequence 315 AA;
Query Match 70.1%; Score 1093; DB 17; Length 315;
Best Local Similarity 80.7%; Pred. No. 5.1e-80;
Matches 213; Conservative 28; Mismatches 23; Indels 0; Gaps 0;
Qy 55 VOTHVAVEQAVVKDATKLEAPVVTGASRGIGKATALGKAGCKVLVNYARSSKEAE 114
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XX
XX 18-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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Query Match 63.18; Score 984; DB 21; Length 308;
Best Local Similarity 65.18; Pred. No. 3e-71;
Matches 207; Conservative 32; Mismatches 65; Indels 14; Gaps 3;

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QY 61 AVEQAVVNDATKLEAPVVVVTGARGIGKATATLALGKAGCKVLVNYARSSKEAEVSKEI 120
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* RESULT 4
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AG35505
ID AAG35505 standard; Protein; 267 AA.
XX AC AAG35505;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 43383.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
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XX PR 20-MAY-1999; 99US-0135124.
XX PR 21-MAY-1999; 99US-0135353.
XX PR 24-MAY-1999; 99US-0135629.
XX PR 25-MAY-1999; 99US-0136021.
XX PR 27-MAY-1999; 99US-0136392.
XX PR 28-MAY-1999; 99US-0136782.
XX PR 01-JUN-1999; 99US-0137222.
XX PR 03-JUN-1999; 99US-0137528.
XX PR 04-JUN-1999; 99US-0137502.
XX PR 07-JUN-1999; 99US-0137724.
XX PR 08-JUN-1999; 99US-0138094.
XX PR 10-JUN-1999; 99US-0138540.
XX PR 10-JUN-1999; 99US-0138847.
XX PR 14-JUN-1999; 99US-0139119.
XX PR 16-JUN-1999; 99US-0139452.
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XX PR 18-JUN-1999; 99US-0139454.
XX PR 18-JUN-1999; 99US-0139455.
XX PR 18-JUN-1999; 99US-0139456.
XX PR 18-JUN-1999; 99US-0139457.
XX PR 18-JUN-1999; 99US-0139458.
XX PR 18-JUN-1999; 99US-0139459.
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Db      174 YAAKGGVISFSFAAREGASRNINNVVCPGFASDMTAEELGDMKKILGTIPLGRYG 233
QY      285 OPEVAGLVEFLALNPAASVMTGQVLTIDGGMVM 318
Db      234 KAEVAGLVEFLALNPAASVITGOAFTIDGGIAL 267

RESULT 5
AAG40275
ID AAG40275 standard; Protein; 273 AA.
XX
AC AAG40275;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49950.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; Genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127482.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 08-OCT-1999; 99US-0158232.
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PR 28-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match      53.6%; Score 835.5; DB 21; Length 232;
Best Local Similarity 71.7%; Pred. No. 28-59;
Matches 170; Conservative 25; Mismatches 29; Indels 13; Gaps 2;

QY 47 RSGRFGSG--VQTHVAAVQAVVVKDQATKLEAFVVTGASRGIGKATALALGKAGCKVLV 104
DB 5 RSRQPFSTSVKQAQATATQSPGEVQVQVSPVVTGASRGIGKATALALGKAGCKVLV 64
QY 105 NYARSSKEAEVYSKEIEAGGGAITFGGDVSKEDADVESMMKKAALDKWGTIDVLVNNAGIT 164
DB 65 NYARSAKEAEVYAKQIEEYGGGAITFGGDVSKATVDVAMKKTALDKWGTIDVLVNNAGIT 124
QY 165 RTLLMRMKKSQWQDVIDLNLGTVFLCTQAAATKVMKKKGGKIIINIASVVGLTGNNVQGAN 224
DB 125 RTLLMRKQSQWQDEVIALNLGTVFLCTQ-----GRLIINISSVVGLTGNNVQGAN 173
QY 225 YSAAGAGVIGFTKTVAREYASRNINVAIAPGFIASDMTAEELGEEKILSTIPIG 281
DB 174 YAAAGGVISFSKTAAREGASRNINVVVCPGFIASDMTAEELGEEKILSTIPIG 230

RESULT 7
ID AAY54422 standard; Protein; 248 AA.
XX AAY54422;
AC AAY54422;
XX
DT 06-APR-2000 (first entry)
DE Amino acid sequence of a beta-ketoacyl-ACP reductase protein.
XX
KW Beta-ketoacyl-ACP reductase; Type II fatty acid synthetase;
KW stereoselectivity; 4-chloroacetoacetic acid ester;
KW (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;
KW beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase;
KW polybeta-hydroxy fatty acid biosynthesis; optically active;
KW 4-halo-3-hydroxybutyric acid ester.
XX
OS Bacillus subtilis.
XX
PN EP955375-A2.
XX
PD 10-NOV-1999.
XX
PF 10-MAY-1999; 99EP-0109403.
XX
PR 08-MAY-1998; 98JP-0126507.
PR 21-OCT-1998; 98JP-0300178.
PR 05-APR-1999; 99JP-0098205.
XX
PA (DAIL ) DAICEL CHEM IND LTD.
XX
PI Yamamoto H;
XX
WPI; 2000-118183/11.
DR N-PSDB; AA245749.
XX
PT Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -
XX
PS Claim 6; Page 19-20; 34pp; English.
XX
CC The present sequence represents a beta-ketoacyl-ACP reductase protein
CC of Bacillus subtilis. The beta-ketoacyl-ACP reductase enzyme constitutes
CC a Type II fatty acid synthetase. The enzyme has an extremely high
CC reducing activity and stereoselectivity towards 4-chloroacetoacetic
CC acid ester. The specification describes a method for producing a
CC (S)-4-halo-3-hydroxybutyric acid ester. The method comprises
CC asymmetrically reducing 4-halo-acetoacetic acid ester or its
CC derivative with beta-ketoacyl-acyl carrier protein reductase
CC constituting Type II fatty acid synthase, or acetoacetyl-CoA
CC reductase constituting the polybeta-hydroxy fatty acid biosynthesis
CC system. The novel method is used to produce optically active
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CC 4-halo-3-hydroxybutyric acid ester, with a high purity.
XX
SQ Sequence 248 AA;
Query Match      46.0%; Score 717.5; DB 21; Length 248;
Best Local Similarity 57.3%; Pred. No. 6.8e-50;
Matches 141; Conservative 47; Mismatches 57; Indels 1; Gaps 1;

QY 73 LEAPVVVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVYSKEIEAGGGAITFGG 132
DB 4 LNDKTAIYTGASRGIGRSIALALAKSGANVVVNYSGNEAKANEVVDIEIKSMGRKAIAVKA 63
QY 133 DVSKEADVESMMKKAALDKWGTIDVLVNNAGITRDITLLMRMKKSQWQDVIDLNLGTVFLCT 192
DB 64 DVSNEPDVQNMKLTSLVFSFTIDVLVNNAGITRDITLLMRMKKEDEWDDVININLKGVFNCT 123
QY 193 QAAATKVMKKRKGKIIINIASVVGLTGNNVQGANYSAAKAGVIGFTKTVAREYASRNINVA 252
DB 124 KAVTRQMMKQSRGRIINVSSTVGVSGNPGQANVYAAKAGVIGLTKSSAKELASRNITVNA 183
QY 253 IAPGFIASDMTAEELGEEKILSTIPIGRYGOPEEVAGLVFEFLAINPAASVMTGQVLTI 312
DB 184 IAPGFISTDMDTKLAKQVQDEMLKQIPLARFGPESDVSVVTFLLA-SGARYMTGQTLHI 242
QY 313 DGGVMV 318
DB 243 DGGVMV 248

RESULT 8
ID ABB48892 standard; Protein; 247 AA.
XX ABB48892;
AC ABB48892;
XX
DT 05-FEB-2002 (first entry)
DE Listeria monocytogenes protein #1596.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-PR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP ) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Psibi H, Dehoux P;
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Pomann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
WPI; 2002-010914/01.
DR
XX
CC Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
CC and prevention of Listeria and related bacterial infections, and
CC related polypeptides -
XX
PS Claim 6; SEQ ID No 1597; 192pp; French.
XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
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Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;

KW antibiotic; antibacterial; drug design.

XX Staphylococcus aureus.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US09180.

XX 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

DR N-PSDB; AAS51824.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

XX Example 3; Seq ID No 5461; 51lpp; English.

XX The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the

CC genes themselves and the discovery of novel antibiotics, the essential

CC genes themselves and the encoded proteins. The prokaryotes used are

CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella

CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The

CC invention is also useful for the identification of potential new targets

CC for antibiotic development. The antisense nucleic acids can also be used

CC to identify proteins used in proliferation, to express these proteins,

CC and to obtain antibodies capable of binding to the expressed proteins.

CC The proteins can be used to screen compounds in rational drug discovery

CC for homologous nucleic acids which are required for cell proliferation in

CC a wide variety of organisms. The present sequence represents an

CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 246 AA;

SQ

Query Match

Best Local Similarity 42.2%; Score 658.5; DB 22; Length 246;

Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;

QY 79 VVTGASRGIGKATALGKAGCKVLVNYARSSKEAEVSEKIEASGEATTFGDDVSKA 138

Db 8 LVTSASRGIGKATALGKAGCKVLVNYARSSKEAEVSEKIEASGEATTFGDDVSKA 67

QY 139 DVESMMKAALDKWGTIDVLVNNAGITRDTLLMRKKSOWODVLDLNTGVFLCTQAAATKV 198

Db 68 EVKAMKEVVSQFGLSDVLVNNAGITRDTLLMRKKEQEDVDVDTNLKGFNCICQATPQ 127

QY 199 MKMKRKGKINIASVGLTGNVGOANYSAKAGVIGTKTVAREYASRNINVAIAPGFI 258

Db 128 MLQRSGAIINLSSVGVAGNPGQANYVATKAGVIGLTKSAARELASRGITVNAVAPGI 187

QY 259 ASDMTAELGELEKXILSTPLRGYQPEVAGLVEFLALNPAASYMTGQVLITDGNVM 318

Db 188 VSDMTDALSELKEQMLTQIFLAFQGDQTDIANTVAFLA-SDKAKYITGTQIHVNGWMY 246

RESULT 13

AAU36530

ID AAU36530 standard; Protein; 246 AA.

XX AAU36530;

XX 14-FEB-2002 (first entry)

XX Staphylococcus aureus cellular proliferation protein #700.

XX Antisense; prokaryotic cellular proliferation protein;

XX antibiotic; antibacterial; drug design.

XX Staphylococcus aureus.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US09180.

XX 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

DR N-PSDB; AAS54389.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

XX Example 3; Seq ID No 12123; 51lpp; English.

XX The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the

CC genes themselves and the discovery of novel antibiotics, the essential

CC genes themselves and the encoded proteins. The prokaryotes used are

CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella

CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The

CC invention is also useful for the identification of potential new targets

CC for antibiotic development. The antisense nucleic acids can also be used

CC to identify proteins used in proliferation, to express these proteins,

CC and to obtain antibodies capable of binding to the expressed proteins.

CC The proteins can be used to screen compounds in rational drug discovery

CC for homologous nucleic acids which are required for cell proliferation in

CC a wide variety of organisms. The present sequence represents an

CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 246 AA;

SQ

Query Match

Best Local Similarity 55.0%; Pred. No. 3.8e-45;

Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;

QY 79 VVTGASRGIGKATALGKAGCKVLVNYARSSKEAEVSEKIEASGEATTFGDDVSKA 138

Db 8 LVTSASRGIGKATALGKAGCKVLVNYARSSKEAEVSEKIEASGEATTFGDDVSKA 67

CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

xx SQ Sequence 246 AA;
Query Match 42.2%; Score 658.5; DB 22; Length 246;
Best Local Similarity 55.0%; Pred. No. 3.8e-45;
Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;
Qy 79 VVTGASRGIGKATLALGKAGCKVLVNVYARSSKEAEVSKIEASGGGEALTFFGGDVSKEA 138
Db 8 LVTGASRGIGESIALQLAEEGYNVAVYAGSKERAEAVVEIKAGVDSPFAIQANVADAD 67
Qy 139 DVESMMKAALDKWTIDVLVNNAGITRDTLLMRMKSQWQDVIDLNLTVGLCTQAAATKV 198
Db 68 EVKAMKEVWSQFGLDVLVNNAGITRDNLLMRMKEQEDVDIDTNLKGVFNCIQKATPQ 127
Qy 199 MMKKRKGKIINIASVGLTGNVGOANYSAKAGVIGTKTVARBYASRNINNVNNAIPGFI 258
Db 128 MLRQRSGAILNLSSVGVAVGNPGQANYVATKAGVIGLTKSAARELASRGITVNAVAFGFI 187
Qy 259 ASDMTAELGEELEKKILSTIPLGRYGOPEEVAGLVEFLALNPAASYMTGOVLITDGGVM 318
Db 188 VSDMTALSDLEKQMLTQIPLARFGQDTDIANTVAFIA-SDKAKYITGQTIHVNGGNYM 246

Search completed: November 7, 2003, 21:02:55
Job time : 53 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 21:02:22 ; Search time 22 Seconds
(without alignments)
611.584 Million cell updates/sec

Title: US-10-024-806-2

Perfect score: 1560

Sequence: 1 MATRAATAAATAAASVSPAARG.....NPAASYMTGQVLTIDGGWVM 318

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pdp.*
- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pdp.*
- 3: /cgn2_6/ptodata/1/iaa/5A-COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/6B-COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/6B-COMB.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1093	70.1	315	3	US-08-793-035-9
2	1093	70.1	315	3	US-08-793-035-9
3	658.5	42.2	246	3	US-09-238-481-2
4	658.5	42.2	246	4	US-09-572-810A-2
5	647.5	41.5	249	4	US-08-134-001C-4825
6	597.5	38.3	243	4	US-09-239-052-2
7	586.5	37.6	255	4	US-08-107-532A-4950
8	573.5	36.8	244	1	US-08-375-962B-13
9	573.5	36.8	244	2	US-08-562-114B-13
10	573.5	36.8	244	3	US-08-729-594A-13
11	573.5	36.8	244	4	US-08-937-933-13
12	565.5	36.2	362	4	US-08-252-991A-18645
13	528	33.8	251	4	US-09-198-452A-309
14	484.5	31.1	262	4	US-09-328-352-4761
15	479.5	30.7	241	4	US-08-178-257-19
16	467.5	30.0	158	4	US-09-724-623-85
17	466.5	29.9	273	6	5512669-4
18	461	29.6	186	4	US-08-858-207A-270
19	457	29.3	246	4	US-08-178-257-9
20	455	29.2	742	4	US-09-252-991A-24489
21	451	28.9	261	4	US-09-468-738A-29
22	451	28.9	261	4	US-09-940-019-29
23	451	28.9	261	4	US-09-940-037A-29
24	450	28.8	436	4	US-08-252-991A-26759
25	439.5	28.2	247	1	US-08-241-766-13
26	426.5	27.3	246	4	US-08-178-257-18
27	423.5	27.1	246	6	5229279-7

Patent No. 5229279
Sequence 5042, Ap
Sequence 28945, A
Sequence 18965, A
Sequence 32380, A
Sequence 7, Appli
Sequence 4512, Ap
Sequence 4431, Ap
Sequence 4805, Ap
Sequence 1, Appli
Sequence 5742, Ap
Sequence 3505, Ap
Sequence 7773, Ap
Sequence 20, Appl
Sequence 28323, A
Sequence 25, Appl
Sequence 24032, A
Sequence 3562, Ap

ALIGNMENTS

RESULT 1

US-08-793-035-9
; Sequence 9, Application US/08793035
; Patent No. 6011201
; GENERAL INFORMATION:
; APPLICANT: Slabas, Antoni R.
; APPLICANT: White, Andrew
; APPLICANT: Chase, Dianne
; APPLICANT: Elborough, Keiran
; APPLICANT: Fentem, Phillip A.
; TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
; TITLE OF INVENTION: Brassica Napus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,035
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9414622.2
; FILING DATE: 20-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB95/01678
; FILING DATE: 17-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-793-035-9

[illegible]

```

RESULT 2
US-08-793-035-10
; Sequence 10, Application US/08793035
; Patent No. 6011201
; GENERAL INFORMATION:
; APPLICANT: Slabas, Antoni R.
; APPLICANT: White, Andrew
; APPLICANT: Chase, Diane
; APPLICANT: Elborough, Keiran
; APPLICANT: Pentem, Phillip A.
; TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
; TITLE OF INVENTION: Brassica Napus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,035
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9414622.2
; FILING DATE: 20-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB95/01678
; FILING DATE: 17-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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US-08-793-035-10

Query Match          70.1%; Score 1093; DB 3; Length 315;
Best Local Similarity 80.7%; Pred. No. 1.6e-101;
Matches 213; Conservative 28; Mismatches 23; Indels 0; Gaps 0;
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Qy	55	VQTHAAVEAQVVKDATKLEAPVVVTGASRGIGKATALGKAGCKVLNVYARSKEAE	114
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Dd	52	VKAQAATAVEQSTGEAVPKVESPVVVVTGASRGIGKALSGLKAGCKVLNVYARSACEAE	111
Qy	115	EVSKEIEASGGEBAITTGGDVSKEADVESMKAAALDKWGTIDVLVNNAGITRDTLLMRKK	174
	:	: : : :	:
Dd	112	EVSQIOEAYGGOAITEGGDVSKEADVEAMKTAIDAAGTTDDVVVNNAGITRDTLLIRMKK	171
Qy	175	SOMODVIDNLNLTGVFLCTQAATVMKKRKGIINIASVVGLTGNTVGQANYSAKAGVIG	234
	:	: : : :	:
Dd	172	SQNDVEDIDLNLTVLCTQAATIKMRRKRGIINIASVVGLTGNIQOANYAAKAGVIG	231
Qy	235	FTKTVAAREASRNINNALPAGFIASDMTAZELGEELEKKILSTPIPLGRYGQPEVAGLVE	294
	:	: : : :	:
Dd	232	FSKTAAREGASRNINNVNCPGFIAADMWAKLGEDMEKKILGTIPLGRYGQPEDVAGLVE	291
Qy	295	FLAINPAASYMTGCVLTIDGMVM	318
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Dd	292	FLAISPAASYITGOAFTIDGGIAI	315

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RESULT 3
US-09-238-481-2
; Sequence 2, Application US/09238481
; Patent No. 6110704
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: FabG
; FILE REFERENCE: GM10192
; CURRENT APPLICATION NUMBER: US/09/238,481
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-238-481-2

Query Match      42.2%; Score 658.5; DB 3; Length 246;
Best Local Similarity 55.0%; Pred. No. 4.4e-58;
Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;

QY    79 VVTGASRGIGKATALAGKAGCKVLVNYAPSSKEAEESVKSEIEASGCEAITFGDYSKEA 138
      :|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB     8 LVTGASRGIGRSIALQLAESGYNAVNYAGSKKAEEAVVEEIKAKGVDSFAIQANVADAD 67
      :|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY    139 DVBSNMKAALDKWGTIDVLVNNAGITRDTLLMEMKKSQWDVIDLNLTVFLCTQAATKV 198
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB     68 EVKAMIKEVVSQGSLDLVLVNNAGITRDNLLMEMKSEQEDWDVDITNLKGVFNCIQAATPQ 127
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY    199 MMKRRGKLINIASVGLTGIVGCQANYSAAKAGVIFTKTVAREYASRNINVNAIAPGI 258
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB     128 MLQRSGAIINTLSVVGAVERNPGQANVATKAGVIGLTSAARELASRGITVNAVAFGI 187
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY    259 ASDMTAELGEELBKILSTIPLCRYGOPERBAGLVFELALNPAAASYWTGCVLATIDGGVMV 318
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB     188 VSMDTALSDELAKQMILTQIPARFGODTDIANTVAFLA--SDRAKYITGQTIIHVGNGWMY 246
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 4
US-09-572-810A-2
; Sequence 2, Application US/09572810A
; Patent No. 6365387
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong

```



```

1  TITLE OF INVENTION:  ACTIVITY, AND WHICH ASSOCIATES WITH P63, A
2  TITLE OF INVENTION:  PORTION OF A RETINOL BINDING PROTEIN RECEPTOR
3  NUMBER OF SEQUENCES:  31
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  Felfe & Lynch
6  STREET:  805 Third Avenue
7  CITY:  New York City
8  STATE:  New York
9  ZIP:  10022
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
12 COMPUTER:  IBM
13 OPERATING SYSTEM:  PC-DOS
14 SOFTWARE:  Wordperfect 5.1 and ASCII
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER:  US/08/562,114B
17 FILING DATE:  22-No. 597264ember-1995
18 CLASSIFICATION:  435
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER:  08/375,962
21 FILING DATE:  20-January-1995
22 ATTORNEY/AGENT INFORMATION:
23 NAME:  Kohli, Vineet
24 REGISTRATION NUMBER:  37,003
25 REFERENCE/DOCKET NUMBER:  LUD 5372.2 CIP
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE:  (212) 688-3200
28 TELEFAX:  (212) 838-3884
29 INFORMATION FOR SEQ ID NO:  13:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH:  244 amino acids
32 TYPE:  amino acid
33 TOPOLOGY:  linear
34 MOLECULE TYPE:  protein
35 FEATURE:
36 NAME/KEY:  E.coli 3-oxoacyl[acyl carrier protein]reductase
37 NAME/KEY:
38 US-08-562-114B-13

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[illegible]

RESULT 10
US-08-729-594A-13
; Sequence 13, Application US/08729594A
; Patent No. 6280997
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH
; TITLE OF INVENTION: CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASE
; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A

TITLE OF INVENTION: RETINOL BINDING PROTEIN RECEPTOR
 NUMBER OF SEQUENCES: 41
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felfe & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/729,594A
 FILING DATE: 11-October-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/562,114
 FILING DATE: 22-No. 6280997ember-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/375,962
 FILING DATE: 20-January-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/258,418
 FILING DATE: 10-June-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6280997man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5372.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 244 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein] reductase
 NAME/KEY:
 US-08-729-594A-13

[illegible]

RESULT 11
US-08-937-993-13
; Sequence 13, Application US/08937993
; Patent No. 6399344

GENERAL INFORMATION:

APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
 TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
 TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski L.L.P.
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 ZIP: 10022

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,993

FILING DATE: September 26, 1997

CLASSIFICATION: 530

Prior APPLICATION DATA:

APPLICATION NUMBER: 08/729,594

FILING DATE: 11-October-1996

Prior APPLICATION DATA:

APPLICATION NUMBER: 08/562,114

FILING DATE: 22-No. 6399344ember-1995

Prior APPLICATION DATA:

APPLICATION NUMBER: 08/375,962

FILING DATE: 20-January-1995

Prior APPLICATION DATA:

APPLICATION NUMBER: 08/258,418

FILING DATE: 10-June-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6399344man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5517

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: E.coli 3-oxoacyl [acyl carrier protein] reductase

NAME/KEY:

US-08-937-993-13

Query Match 36.8%; Score 573.5; DB 4; Length 244;

Best Local Similarity 49.4%; Pred. No. 1.5e-49;

Matches 121; Conservative 45; Mismatches 74; Indels 5; Gaps 3;

Qy 74 EAPVVVTGASRGIGKATALLGKAGCKVLVNYARSKAEVSKIEASGGEAITFGGD 133

Db 4 EGKIALVTGASRGIGRAIAETLAARGKV-IGTATSENGAQAI SDYLGA NGKGLML--N 59

Qy 134 VSKEADVESNMKAALDKWGTIDVLVNNAGITRDITLLMRMKSQWQVVIDNLNLTGVFLCTQ 193

Db 60 VTDPAESVLEKTRAEFGEVDILVNNAGITRDITLLMRMKSQWQVVIDNLNLTGVFLCTQ 193

Qy 194 AATKVMKKRKGKINTASVVLGNVGOANYSAAGVIGFTKTIVAREVASRNINVAI 253

Db 120 AVWEAMKKRGRITITGVSVGTWNGGQANYAAKAGLGFSGSLAREVASRGITVNVV 179

Qy 254 APGTIASDMTAELEKILSTIPLGRYQGPVEVAGLVFELALNPAASVMTGOVLITD 313

Db 180 APGTIDMTALSDQDQAGILAVPAGRLGGAQEI ANAVAFASDEAA-YITGETLHVN 238

Qy 314 GGMVM 318

Db 239 GGMVM 243

RESULT 12

US-09-252-991A-18645

; Sequence 18645; Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 18645

; LENGTH: 362

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

; US-09-252-991A-18645

Query Match 36.2%; Score 565.5; DB 4; Length 362;

Best Local Similarity 42.6%; Pred. No. 1.7e-48;

Matches 130; Conservative 54; Mismatches 108; Indels 13; Gaps 3;

Qy 14 SSPAARGAAGAAAARRRGFTVFGGAARPSPTLRSRGSGVQTHVAAVQAVKDATKL 73

Db 70 SAGRAASWQASTGAARASIPMAWMASSRRSPRAP-----PWPBREGKGNPMSL 118

Qy 74 EAPVVVTGASRGIGKATALLGKAGCKVLVNYARSKAEVSKIEASGGEAITFGGD 133

Db 119 QGKVALVTGASRGIGQAIALLELGLGA-VVIGTATSASGAETKATLKVNGVSGAGLVLD 177

Qy 134 VSKEADVESNMKAALDKWGTIDVLVNNAGITRDITLLMRMKSQWQVVIDNLNLTGVFLCTQ 193

Db 178 VSSDESVAATLEHIQOHLGQPLIVVNNAGITRDITLLMRMKSQWQVVIDNLNLTGVFLCTQ 237

Qy 194 AATKVMKKRKGKINTASVVLGNVGOANYSAAGVIGFTKTIVAREVASRNINVAI 253

Db 238 AVLRGMTKARWGRITITGVSVGTWNGGQANYAAKAGLGFTRALAREVGSRAITVNAV 297

Qy 254 APGTIASDMTAELEKILSTIPLGRYQGPVEVAGLVFELALNPAASVMTGOVLITD 313

Db 298 APGTIDMTRELPEAQREALLGQIPLGRGQAEEIAKVVGFLA-SDGAAVVTGATVPVN 356

Qy 314 GGMVM 318

Db 357 GGMVM 361

RESULT 13

US-09-198-452A-309

; Sequence 309; Application US/09198452A

; Patent No. 6552994

; GENERAL INFORMATION:

; APPLICANT: Griffiths, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmer

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 309

; LENGTH: 251

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

; US-09-198-452A-309

Query Match 33.8%; Score 528; DB 4; Length 251;

Best Local Similarity 46.4%; Pred. No. 5,7e-45;
Matches 111; Conservative 41; Mismatches 85; Indels 2; Gaps 2;

Qy 78 VVVTGASRGIGKATALGKAGCKVLYNVARSSKEAEVSKIEBASGCEAITFGDVSKE 137
Db 13 VIVTGGSRGIGLIGVVKLPLENGADVEI-WGLNEERGQAVIESLTGLGGEVSFARVDVSHN 71

Qy 138 ADVESMMKAALDKNGTIDVLVNNAGITDITLLMRMKSQWQDVLDNLITGVFLCTQATK 197
Db 72 GGVKDCVCFKDKNKVDILVNNAGITDITLLMRMSEDDWQSVISTNLSLYTTCSSVIR 131

Qy 198 VMKRRKGKIINIASVVLGTNGVQANYSAKAGVIGTKTVAREYASRNINVAIAPGF 257
Db 132 HMIKARSGIINVASIVAKIGSAGQTYAAKAGIATKSLAKEVAARNIRVNCIAPGF 191

Qy 258 IASDWTAEHLGELEKILSTPIGRYQPEVAGLVEFLALNPAASYMTQVLTIDGM 316
Db 192 IETDMSVINDLKAELKSLPLGRAGTFEDVARVALFLA-SQLSSYMTAQTLVVDGGL 249

RESULT 14
US-09-328-352-4761
; Sequence 4761, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03FA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4761
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4761

Query Match 31.1%; Score 484.5; DB 4; Length 262;
Best Local Similarity 42.9%; Pred. No. 1.4e-40;
Matches 108; Conservative 51; Mismatches 86; Indels 7; Gaps 4;

Qy 68 KDATKLEAPVVVTGASRGIGKATALGKAGCKVLYNVARSSKEAEVSKIEI-EASGGE 126
Db 16 KNCMTQERKVALVTGASRGIGAAIAQOLIQGYFV-VGTATSESGAKRLTDSFGQAGL 74

Qy 127 AITFGGVSKEADVESMMKAALDKNGTIDVLVNNAGITDITLLMRMKSQWQDVLDNLIT 186
Db 75 AL-----DVRNLDETEAVVSHIEQYGPVLVNNAGITKDNLLRMSDEDDWDDILNIHLK 130

Qy 187 GVFLCTQAAATKVMKRRKGKIINIASVVLGTNGVQANYSAKAGVIGTKTVAREYASR 246
Db 131 AVTLRSRVUKMTKARFGRILINSSVVAHFANPGQANYSAKAGIABAFERSLAKENGSR 190

Qy 247 NINVNIAIAPGFASDWTAEHLGELEKILSTPIGRYQPEEVLALNPAASYMT 306
Db 191 QITVNSVAPGFATENTDALSIEDIRKMSQVALNRLGEPQDIANAVFLA-SDKAGIIT 249

Qy 307 GOVLITDGGMM 318
Db 250 GTVLHVNGLYM 261

RESULT 15
US-08-178-257-19
; Sequence 19, Application US/08178257
; Patent No. 6515205
; GENERAL INFORMATION:
; APPLICANT: LIEBERGSELL, MATTHIAS
; APPLICANT: STEINBUCHER, ALEXANDER
; TITLE OF INVENTION: PRODUCTION OF POLYALKANOATE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN, DABY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,257
FILING DATE: 11-JAN-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01291
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9115245.4
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 9320/206058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
TELEFAX: 202/822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Zoogloea ramigera
US-08-178-257-19

Query Match 30.7%; Score 479.5; DB 4; Length 241;
Best Local Similarity 45.2%; Pred. No. 3.9e-40;
Matches 109; Conservative 47; Mismatches 76; Indels 9; Gaps 6;

Qy 77 VVVTGASRGIGKATALGKAGCKVLYNVARSSKEAEVSKIEBASGCEAITFGDVSKE 136
Db 4 VALVTGSGRGIGAAISIALKAAGYKVAASYAGN-----DDAAKPFKAETGLAV-YKMDVSS 58

Qy 137 -EADVESMMKAALDKNGTIDVLVNNAGITDITLLMRMKSQWQDVLDNLITGVFLCTQAA 195
Db 59 YEACVGIKVEAD-LGPDIDLVLVNNAGITKDMFHKMTDPMNAVINTNLGLFNMTHPV 117

Qy 196 TKVMKRRKGKIINIASVVLGTNGVQANYSAKAGVIGTKTVAREYASRNINVAIAP 255
Db 118 WSGMRDRSFGRIVNISSINGKQGMQGMQANYSAKAGDLGFTKALAQEAGKAGITVAICP 177

Qy 256 GFTASDWTAEHLGELEKILSTPIGRYQPEVAGLVEFLALNPAASYMTQVLTIDG 314
Db 178 GYIGTEMVRAIPEKVLNERIIPQIPVGLRGEPEIARIIVVFLA-SDEAGFITGTSISANG 236

Qy 315 G 315
Db 237 G 237

Search completed: November 7, 2003, 21:05:29
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 21:04:32 ; Search time 49 seconds
(without alignments)
1114.618 Million cell updates/sec

Title: US-10-024-806-2
Perfect score: 1560
Sequence: 1 MATAAATAAAAVSSPAARG.....NPAAASYMTGQVLTDGGMW 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1560	100.0	318	12	US-10-024-806-2
2	1279	82.0	312	12	US-10-024-806-4
3	1128	72.3	320	12	US-10-024-806-6
4	986.5	63.2	299	12	US-10-024-806-8
5	658.5	42.2	246	9	US-09-815-242-5461
6	658.5	42.2	246	9	US-09-815-242-12123
7	658.5	42.2	246	9	US-09-815-242-12803
8	598.5	38.4	245	9	US-09-815-242-13100
9	597.5	38.3	243	9	US-09-815-242-10921
10	597.5	38.3	243	9	US-09-815-242-13360
11	597.5	38.3	243	9	US-09-815-242-13561
12	576.5	37.0	244	9	US-09-815-242-10126
13	573.5	36.8	244	11	US-09-849-092-13
14	556	35.6	247	9	US-09-815-242-11893
15	545.5	35.0	242	9	US-09-815-242-10974

16	529	33.9	247	10	US-09-479-040-9	Sequence 9, Appli
17	528	33.8	239	15	US-10-156-761-13989	Sequence 13989, A
18	496.5	31.8	247	9	US-09-815-242-11342	Sequence 11342, A
19	486.5	31.2	247	9	US-09-815-242-11514	Sequence 11514, A
20	478.5	30.7	313	15	US-10-156-761-11190	Sequence 11190, A
21	467.5	30.0	158	12	US-10-288-930-85	Sequence 85, Appl
22	459	29.4	237	9	US-09-823-901-2	Sequence 2, Appli
23	459	29.4	237	15	US-10-175-696-14	Sequence 14, Appl
24	458	29.4	253	15	US-10-156-761-14536	Sequence 14536, A
25	457	29.3	240	12	US-10-166-225A-179	Sequence 179, App
26	451	28.9	261	10	US-09-940-037A-29	Sequence 29, Appl
27	450	28.8	226	10	US-09-895-913A-362	Sequence 362, App
28	448.5	28.7	253	9	US-09-815-242-10279	Sequence 10279, A
29	447	28.7	261	12	US-10-004-115A-36	Sequence 36, Appl
30	447	28.7	261	12	US-10-327-108-12	Sequence 12, Appl
31	444.5	28.5	261	15	US-10-187-267A-33	Sequence 33, Appl
32	441.5	28.3	253	9	US-09-815-242-13878	Sequence 13878, A
33	433.5	27.8	641	10	US-09-364-847-10	Sequence 10, Appl
34	433	27.8	642	10	US-09-364-847-59	Sequence 59, Appl
35	426.5	27.3	246	10	US-09-364-847-6	Sequence 6, Appl
36	426.5	27.3	641	10	US-09-364-847-19	Sequence 19, Appl
37	426.5	27.2	642	10	US-09-364-847-61	Sequence 61, Appl
38	424.5	27.2	243	12	US-10-238-075-837	Sequence 837, App
39	423.5	27.1	259	10	US-09-931-186-17	Sequence 17, Appl
40	417.5	26.8	906	14	US-10-060-230-19	Sequence 19, Appl
41	417.5	26.8	906	14	US-10-060-230-20	Sequence 20, Appl
42	411.5	26.4	315	15	US-10-156-761-13732	Sequence 13732, A
43	411.5	26.4	906	14	US-10-060-230-21	Sequence 21, Appl
44	411.5	26.4	906	14	US-10-060-230-22	Sequence 22, Appl
45	402	25.8	261	10	US-09-971-536-74	Sequence 74, Appl

ALIGNMENTS

RESULT 1
US-10-024-806-2
; Sequence 2, Application US/10024806
; Publication No. US20030167532A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping
; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; TITLE OF INVENTION: Their use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/258,417
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Zea mays
US-10-024-806-2

Query Match 100.0%; Score 1560; DB 12; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-130;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MATAAATAAAAVSSPAARGAAGAAASRRGFTVFGGAARFPTLRSRGFGSGVTHVA	60
DB	1	MATAAATAAAAVSSPAARGAAGAAASRRGFTVFGGAARFPTLRSRGFGSGVTHVA	60
QY	61	AVEQAVVKKATKLEAPVVVVVTGASRGIGKATALALGKAGCKVLVNVARSKEAEVSK	120
DB	61	AVEQAVVKKATKLEAPVVVVVTGASRGIGKATALALGKAGCKVLVNVARSKEAEVSK	120
QY	121	EASGGGAITFGGDVSKAEADVSMKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWDV	180
DB	121	EASGGGAITFGGDVSKAEADVSMKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWDV	180


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Qy 181 IDLNLGTGVLCTQATKVMKKRKKIINIASVVLGNVGOQANYSAAGVIGFTKVA 240
Db 181 IDLNLGTGVLCTQATKVMKKRKKIINIASVVLGNVGOQANYSAAGVIGFTKVA 240
Qy 241 REYASRNINVAIAPGFTASDMTAELEKILSTIPLGRYQOPEVAGLVEFLALNP 300
Db 241 REYASRNINVAIAPGFTASDMTAELEKILSTIPLGRYQOPEVAGLVEFLALNP 300
Qy 301 AASYMTGQVLTIIDGGVM 318
Db 301 AASYMTGQVLTIIDGGVM 318

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RESULT 2
US-10-024-806-4
; Sequence 4, Application US/10024806
; Publication No. US20030167532A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; FILE OF INVENTION: Their Use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/258,417
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Zea mays
US-10-024-806-4

```

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Query Match 82.0%; Score 1279; DB 12; Length 312;
Best Local Similarity 82.0%; Pred. No. 1.7e-105;
Matches 264; Conservative 20; Mismatches 20; Indels 18; Gaps 3;

Qy 4 AAATAAAAVSSPAARGAAGAAASRRGFVTFGGGAARFSPILSRGRCFS-----GVQ 56
Db 2 AAATAAAALASPLG-----STSLARRGLVS-----FAPALRPPDRSRVALLGVR 50

Qy 57 THVAAVEQAVVYKDATKLEAPVVTGASRGIGKATATGALGKAGCKVLVNYARSSKEAEV 116
Db 51 THVTAVDQAVVYKDTKLEGPVVVTGASRGIGKATATGALGKAGCKVLVNYARSSKEAEV 110

Qy 117 SKKEIEASGGEAITFGGDVSKADVESMMKALDKWGTIDVLVNNAGITRDITLLMRKSK 176
Db 111 SKKEIEASGGEAITFGGDVSKADVESMLKVAVDTWGTIDVLVNNAGITRDITLLMRKSK 170

Qy 177 WQDVIDLNLGTGVLCTQATKVMKKRKKIINIASVVLGNVGOQANYSAAGVIGFT 236
Db 171 WQDAIDLNLGTGVLCTQATKVMKKRKKIINIASVVLGNVGOQANYSAAGVIGFT 230

Qy 237 KTVAEYASRNINVAIAPGFIASDMTAELEKILSTIPLGRYQOPEVAGLVEFL 296
Db 231 KTVAEYASRNINVAIAPGFIASDMTAELEKILSTIPLGRYQOPEVAGLVEFL 290

Qy 297 ALNPAASVMTGQVLTIIDGGVM 318
Db 291 ALSPAASVITGQVLTIIDGGVM 312

```

```

RESULT 3
US-10-024-806-6
; Sequence 6, Application US/10024806
; Publication No. US20030167532A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping

```

```

; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; FILE OF INVENTION: Their Use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/258,417
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Glycine max
US-10-024-806-6

```

```

Query Match 72.3%; Score 1128; DB 12; Length 320;
Best Local Similarity 72.2%; Pred. No. 4.7e-92;
Matches 234; Conservative 29; Mismatches 43; Indels 18; Gaps 3;

Qy 8 AAAAASVSSPAARGAAGAAASRRGFVTFGGGAARFSPILSRGRCFS-----RSGRGF--SG 54
Db 2 ASIAGSNVCLRTANFGASGRK-----IGQIRQWSPILTNLRPVSGLRHSNTFPSSSG 56

Qy 55 VOTHVAVEQAVVYKDATKLEAPVVTGASRGIGKATATGALGKAGCKVLVNYARSSKEAE 114
Db 57 VRAQVATLEEAGTGATOKVEAPVAVVTGASRGIGKATATGALGKAGCKVLVNYARSSKEAE 116

Qy 115 EVSKEIEASGGEAITFGGDVSKADVESMMKALDKWGTIDVLVNNAGITRDITLLMRK 174
Db 117 EVSKEIEASGGEAITFGGDVSKADVESMLKTAVDWTGIDVLVNNAGITRDITLLMRK 176

Qy 175 SQWQDVIDLNLGTGVLCTQATKVMKKRKKIINIASVVLGNVGOQANYSAAGVIG 234
Db 177 SQWQDVIDLNLGTGVLCTQAAKIMMKKKGRIVNIASVVLGNVGOQANYSAAGVIG 236

Qy 235 FTKTVAEYASRNINVAIAPGFIASDMTAELEKILSTIPLGRYQOPEVAGLVE 294
Db 237 LTKTVAEYASRNITVNAVAPGFIASDMTAKLGODIEKKILETIPLGRYQOPEVAGLVE 296

Qy 295 FLALNPAASVMTGQVLTIIDGGVM 318
Db 297 FLALNQAAASVITGQVFTIDGGVM 320

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RESULT 4
US-10-024-806-8
; Sequence 8, Application US/10024806
; Publication No. US20030167532A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping
; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; FILE OF INVENTION: Their Use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/258,417
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Glycine max
US-10-024-806-8

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Query Match 63.2%; Score 986.5; DB 12; Length 299;
Best Local Similarity 71.2%; Pred. No. 1.6e-79;
Matches 205; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

Qy 32 FVTFGGGAARFSPILSRGRCFSGVQTHAAVEQAVVYKDATK-LEAPVVTGASRGIGKA 90

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Db 12 FRTKGPARKVPSQVLAFORSNSNGSPSPSEQLLEASQKNMEAPVVVTGASRGIGRA 71
QY 91 TALALGAGCKVLVNYARSKAEAEVSKETIASGGEHAITFGGDVSKADVESMMKAALDK 150
Db 72 IALLSLGAPCKVLVNYARSMQAEVSNLIEAFGGQALTPEGDVSNEADVESMIRTAEDA 131
QY 151 WGTIDVLNNAGITRDITLLMRMKSQMDVIDNLNLTGVFLCTQATKVMKKKGGKIINI 210
Db 132 WGTIDVLNNAGITRDITLLMRMKSQMDVIDNLNLTGVFLCTQATKVMKKKGGKIINI 191
QY 211 ASVVGLTGNVQOANYSAAGKAGVIGFTKTVAEYASRNINVAAPGFIASDMTAEICEEL 270
Db 192 TSVIGQVGNVQOANYSAAGKAGVIGFTKTVAEYASRNITVNAVAPGFIASDMTANLRPGI 251
QY 271 EKKILSTIPIGRGQPEEAGLVEFLALNPAASVMTQVLTIDGGMVM 318
Db 252 EKKRLEIPIGRIGQPEEAGLVEFLALNPAASVMTQVLTIDGGLAM 299

RESULT 5

US-09-815-242-5461
; Sequence 5461, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5461
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5461

Query Match 42.2%; Score 658.5; DB 9; Length 246;
Best Local Similarity 55.0%; Pred. No. 1.6e-50;
Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;
QY 79 VVTGASRGIGKATATLALGKAGCKVLVNYARSKAEAEVSKETIASGGEHAITFGGDVSKEA 138
Db 8 LVTGASRGIGRSIALQLAEBGVNVAANYAGSKEAEVVEIKAKGVDSFAIQANVADAD 67
QY 139 DVESMMKAALDKWGTIDVLNNAGITRDITLLMRMKSQMDVIDNLNLTGVFLCTQATKV 198
Db 68 EVKAMIKVVSQFSGSLDVLNNAGITRDITLLMRMKEQEMDDVIDITNLKGVFNFCIQKATPQ 127
QY 199 MMKRRGKIINIASVSVGLTGNVQOANYSAAGKAGVIGFTKTVAEYASRNINVAAPGFI 258

Db 128 MURQSGALINSSVVGAVNPGQANYVATKGVIGLITKSAARELASRGITVNAVAPGFI 187
QY 259 ASDMTAEELGEELEKKILSTIPIGRGQPEEAGLVEFLALNPAASVMTQVLTIDGGMVM 318
Db 188 VSDMTDALSDELKQEWLTQIPLARFGQDITDIANTVAFILA-SDKAKYITGQTIHVNGGMVM 246

RESULT 6

US-09-815-242-12123
; Sequence 12123, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12123
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12123

Query Match 42.2%; Score 658.5; DB 9; Length 246;
Best Local Similarity 55.0%; Pred. No. 1.6e-50;
Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;
QY 79 VVTGASRGIGKATATLALGKAGCKVLVNYARSKAEAEVSKETIASGGEHAITFGGDVSKEA 138
Db 8 LVTGASRGIGRSIALQLAEBGVNVAANYAGSKEAEVVEIKAKGVDSFAIQANVADAD 67
QY 139 DVESMMKAALDKWGTIDVLNNAGITRDITLLMRMKSQMDVIDNLNLTGVFLCTQATKV 198
Db 68 EVKAMIKVVSQFSGSLDVLNNAGITRDITLLMRMKEQEMDDVIDITNLKGVFNFCIQKATPQ 127
QY 199 MMKRRGKIINIASVSVGLTGNVQOANYSAAGKAGVIGFTKTVAEYASRNINVAAPGFI 258
Db 128 MURQSGALINSSVVGAVNPGQANYVATKGVIGLITKSAARELASRGITVNAVAPGFI 187
QY 259 ASDMTAEELGEELEKKILSTIPIGRGQPEEAGLVEFLALNPAASVMTQVLTIDGGMVM 318
Db 188 VSDMTDALSDELKQEWLTQIPLARFGQDITDIANTVAFILA-SDKAKYITGQTIHVNGGMVM 246

RESULT 7

US-09-815-242-12803
; Sequence 12803, Application US/09815242
; Patent No. US20020061569A1

```

; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13100
; LENGTH: 246
; TYPE: PR1
; ORGANISM: Staphylococcus aureus
; US-09-815-242-13100

Query Match 42.2%; Score 658.5; DB 9; Length 246;
Best Local Similarity 55.0%; Pred. No. 1.6e-50;
Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;

QY 79 VVTGASRGIGKATALGKAGCKLVNVARSKAEVSKIEASGEAIFGDDVSKEA 138
Db 8 LVTGASRGIGRSIALQAEAGYNAVYAGSKAEAVVEIKAGVDSFAIQANVADAD 67
QY 139 DVESMMKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWQDVLDNLGTGVLCTQAATKV 198
Db 68 EVKAMKEVVSQFSGSLDVLVNNAGITRDNLLMRKKEQWDDVIDNLKGVFNCIQKATPQ 127
QY 199 MMKRGKGIINIASVVLGTGNVQANYSAKAGVIGFTKTVAREYASRNINVAIAPGFI 258
Db 128 MLRQSGAIINLSSVVGAVGNPGQANYVATKAGVIGLTKSAARELASRGITVNAVAPGFI 187
QY 259 ASDMTAEELGEEKILSTIPIGRYQGPVEVAGLVEFLALNPAASVMTGQVLITDGGVM 318
Db 188 VSDMTDALSDELKEQMLTQIPLARFGQDITANTVAFIA-SDKAKYITGQTHVNGGMYM 246

RESULT 9
US-09-815-242-10921
; Sequence 10921, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12803
; LENGTH: 246
; TYPE: PR1
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12803

Query Match 42.2%; Score 658.5; DB 9; Length 246;
Best Local Similarity 55.0%; Pred. No. 1.6e-50;
Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;

QY 79 VVTGASRGIGKATALGKAGCKLVNVARSKAEVSKIEASGEAIFGDDVSKEA 138
Db 8 LVTGASRGIGRSIALQAEAGYNAVYAGSKAEAVVEIKAGVDSFAIQANVADAD 67
QY 139 DVESMMKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWQDVLDNLGTGVLCTQAATKV 198
Db 68 EVKAMKEVVSQFSGSLDVLVNNAGITRDNLLMRKKEQWDDVIDNLKGVFNCIQKATPQ 127
QY 199 MMKRGKGIINIASVVLGTGNVQANYSAKAGVIGFTKTVAREYASRNINVAIAPGFI 258
Db 128 MLRQSGAIINLSSVVGAVGNPGQANYVATKAGVIGLTKSAARELASRGITVNAVAPGFI 187
QY 259 ASDMTAEELGEEKILSTIPIGRYQGPVEVAGLVEFLALNPAASVMTGQVLITDGGVM 318
Db 188 VSDMTDALSDELKEQMLTQIPLARFGQDITANTVAFIA-SDKAKYITGQTHVNGGMYM 246

RESULT 8
US-09-815-242-13100
; Sequence 13100, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A

```

```

; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10921
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10921

Query Match      38.4%; Score 598.5; DB 9; Length 245;
Best Local Similarity 52.3%; Pred. No. 3.5e-45;
Matches 126; Conservative 42; Mismatches 68; Indels 5; Gaps 2;

QY 78 VVVTGSRGIGKATATAGAGCKVLVNVARSSKEAEVSKTEASGGRAITPGGDSKE 137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 VFTGSTRGIGKAVAFKAGANIVLN--GRSEITPEQRFQTEAFGVKICGLSGDISDF 65

QY 138 ADVESMMKAALDKWGTIDVLNNAGITRDTLLMRMKSQWQDVIDLNLGTVLCTQAATK 197
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 DAAGEMIQTAVDQGSIDILVNNAGITNDKLLRMTKEDFNACDINLVGTFTNMTQAAVK 125

QY 198 VMKKRKGKIINIASVVGLTGNVGOANYSAAGAGVIGFTKTVAREYASRNINVAIAPGF 257
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 RMKQSSGRIINWASVGLMGNVGOANYAASKAGVGVGFTKSVAREVAPRGITCNAIAPGF 185

QY 258 IASDWTAEELGEELEKKILSTIPLGRYGOPBEVAGLVEFLALNPAASVMTGQVLTIDGGMV 317
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 186 IQTMDTVLSEKVKTKQNAQIPLQTEQVEDVAATAIFLAKSP---YITGQVNVVDGGLV 242

QY 318 M 318
Db 243 M 243

RESULT 10
US-09-815-242-13360
; Sequence 13360, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13360
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13581

Query Match      38.3%; Score 597.5; DB 9; Length 243;
Best Local Similarity 50.6%; Pred. No. 4.3e-45;
Matches 126; Conservative 48; Mismatches 66; Indels 9; Gaps 3;

QY 72 KLEAPVVVVTGSRGIGKATATAGAGCKVLVNVARSSKEA--EVSKEIEASGGEAIT 129
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 KLEHKNIFITGSSRGIGLAIAHKFAQAGANIVLN----SRGAISELLAEFNSYGIKVP 57

QY 130 FGGDSKEADVESMMKAALDKWGTIDVLNNAGITRDTLLMRMKSQWQDVIDLNLGTVF 189
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 ISGDSVDFADAKMTDQAIAGELSGVDVLVNNAGITQDILMLKNTADFKVILKNITGAF 117

QY 190 LCTQAAATKVMKKRKGKIINIASVVGLTGNVGOANYSAAGAGVIGFTKTVAREYASRNIN 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 118 NMTQSVLKPMKAREGAIINMSSVVGLMGNVGOANYAASKAGLIGFTKSVAREVASNRIR 177

QY 250 VNAIAPGFTASDWTAEELGEELEKKILSTIPLGRYGOPBEVAGLVEFLALNPAASVMTGQV 309
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 VNVIAFGMIESDMTAILSDKIEATLAQIPMKBFQAEQVADLTVPFLA---GQDYLITGV 234

QY 310 LTIDGGMV 318
Db 235 IADGGLSM 243

RESULT 11
US-09-815-242-13581
; Sequence 13581, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13581
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13581

Query Match      38.3%; Score 597.5; DB 9; Length 243;
Best Local Similarity 50.6%; Pred. No. 4.3e-45;
Matches 126; Conservative 48; Mismatches 66; Indels 9; Gaps 3;
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Search completed: November 7, 2003, 21:09:56
Job time : 50 secs

Db 226 NYSAAKAGVIGTKTVAREYASRNINNVAVPGFTSSDWTSKLGGDDINKKILETIPLGRY 285
 QY 284 GQPEVAGLVFELALNPAASTWGTQVLTIDGGVM 318
 Db 286 GQPEVAGLVFELALNPASSVYTGQVFTIDGGMTM 320

RESULT 2
 S22416
 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 11-Jun-1999
 C;Accession: S22416
 R;Slabas, A.R.; Chase, D.; Nishida, I.; Murata, N.; Sidebottom, C.; Safford, R.; Sheldon
 Biochem. J. 283: 321-326, 1992
 A;Title: Molecular cloning of higher-plant 3-oxoacyl-(acyl carrier protein) reductase. S
 as Asn, CCC for residue 256 as Ala, AAA for residue 286 as Arg, and CCT for residue 301
 A;Reference number: S22416; MUID:92246853; PMID:1575676
 A;Accession: S22416
 A;Molecule type: mRNA
 A;Residues: 1-319 <SLA>
 A;Cross-references: EMBL:X64464; NID:gl6204; PIDN:CAA45794.1; PID:gl6205
 A;Note: the authors translated the codon CTT for residue 33 as Ile, CGA for residue 44 a
 C;Genetics:
 A;Genome: nuclear
 C;Function:
 A;Pathway: fatty acid biosynthesis
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 F;1-59/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F;60-319/Product: 3-oxoacyl-(acyl-carrier-protein) reductase #status predicted <NAT>
 F;77-257/Domain: short-chain alcohol dehydrogenase homology <SADH>
 F;226/Active site: Tyr #status predicted

Query Match 66.1%; Score 1030.5; DB 2; Length 319;
 Best Local Similarity 67.4%; Pred. No. 3.2e-61;
 Matches 215; Conservative 36; Mismatches 63; Indels 5; Gaps 4;

QY 4 AAATAAAAVSSPAARGAAGAAASR-RGFTVFGGGAARFSP-TLRSRGFSG--VQTHV 59
 Db 2 AAATAAAVSLKAV-GKLGFRFISQIQLAPLHSAIPHFGMLRCRSPFSTSVVKAQA 60
 QY 60 AAQVAVKQATKLEAPVAVVTGASRGIGKATATLALGKAGCKVLNVYARSKEAEVSKE 119
 Db 61 TATEQSPGVQVQVSPVVTGASRGIGKATATLALGKAGCKVLNVYARSKEAEVAKQ 120
 QY 120 IEASGGAITFGDVSKEADVSMKKAALDKWGTIDVLVNNAGITRDTLLMRMKSQWQD 179
 Db 121 IEYGGQAITFGDVSKEATVDVAMMTALDKWGTIDVLVNNAGITRDTLLMRMKSQWDE 180
 QY 180 VIDNLGTVFLCTCAATKVMKKKGIINIASVVGITGNVGOANYSAAGVIGFTKTV 239
 Db 181 VIDNLGTVFLCTCAATKVMKKKGIINIASVVGITGNVGOANYSAAGVIGFTKTV 240
 QY 240 AREYASRNINNVAVPGFTSSDWTAELEKEKILSTIPLGRYQPEEVLALNP 299
 Db 241 AREGASRNINNVVCPGFIASDMTAELEGELEKILSTIPLGRYQPEEVLALNP 300
 QY 300 PAASYMTGOVLTIDGGVM 318
 Db 301 PAASYITGOAFTIDGGIAI 319

RESULT 3
 A86378
 Protein F21J9.2 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 01-Mar-2002
 C;Accession: A86378
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Mazzial
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: A86378
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-308 <STO>
 A;Cross-references: GB:AE005172; NID:g9743327; PIDN:AAF97951.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 63.1%; Score 984; DB 2; Length 308;
 Best Local Similarity 65.1%; Pred. No. 3.8e-58;
 Matches 207; Conservative 32; Mismatches 65; Indels 14; Gaps 3;

QY 4 AAATAAAAVSSPAARGAAGAAASR-RGFTVFGGGAARFSP-TLRSRGFSG--VQTHV 60
 Db 2 AAATAAAVSLKAV-KLGFREISQIQLAPLHSAIPHFGMLRCRSPFSTSVVKAQA 61
 QY 61 AVEQAVKQATKLEAPVAVVTGASRGIGKATATLALGKAGCKVLNVYARSKEAEVSKEI 120
 Db 62 ATEQSPGVQVQVSPVVTGASRGIGKATATLALGKAGCKVLNVYARSKEAEVAKQI 121
 QY 121 EASGGAITFGDVSKEADVSMKKAALDKWGTIDVLVNNAGITRDTLLMRMKSQWQD 180
 Db 122 EYGGQAITFGDVSKEATVDVAMMTALDKWGTIDVLVNNAGITRDTLLMRMKSQWDE 181
 QY 181 IDNLGTVFLCTCAATKVMKKKGIINIASVVGITGNVGOANYSAAGVIGFTKTV 240
 Db 182 IDNLGTVFLCTQ-----GRIINISSVVGITGNVGOANYSAAGVIGFTKTV 230
 QY 241 REYASRNINNVAVPGFTSSDWTAELEKEKILSTIPLGRYQPEEVLALNP 300
 Db 231 REGASRNINNVVCPGFIASDMTAELEGELEKILSTIPLGRYQPEEVLALNP 290
 QY 301 PAASYMTGOVLTIDGGVM 318
 Db 291 PAASYITGOAFTIDGGIAI 308

RESULT 4
 T00667
 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) F316.30 - Arabidopsis thaliana
 N;Alternate names: beta-oxoacyl-(acyl carrier protein); protein F316.30
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 29-Oct-1999
 C;Accession: T00667
 R;Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Arau
 J; Vysotskaia, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
 submitted to the EMBL Data Library, February 1998
 A;Reference number: Z14197
 A;Accession: T00667
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-270 <FED>
 A;Cross-references: EMBL:AC002396; NID:g2749918; PIDN:AA00590.1; FID:g28882; GSPDB:GN

C;Genetics:
 A;Map position: 1
 A;Introns: 55/1; 102/3; 120/3; 147/3; 163/1; 194/3; 239/3
 A;Function: fatty acid biosynthesis
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C;Keywords: fatty acid biosynthesis; NADP; oxidoreductase
 F;77-246/Domain: short-chain alcohol dehydrogenase homology <SADH>
 Query Match 53.3%; Score 832; DB 2; Length 270;

QY 311 TIDGGVMV 318
:
Db 239 NVDGVMV 246

RESULT 6
AH2042
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
R;Accession: AH2042
C;Kaneoko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigun
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A;/title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A
A;/Reference number: AB1807; UID:21595285; PMID:11759840
A;/Experimental source: strain PCC 7120
A;/Molecule type: DNA
A;/Status: preliminary
A;/Residues: 1-251 <CUR>
A;/Cross-references: GB:BA000019; PIDN:BAB73593.1; PID:g17130984; GSPDB:GN00179
A;/Experimental source: strain PCC 7120
C;Genetics:
A;/Gene: fabG
C;/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 50.9%; Score 794.5; DB 2; Length 251;
Best Local Similarity 65.0%; Pred. No. 1.le-45;
Matches 160; Conservative 30; Mismatches 53; Indels 3; Gaps 1;

QY 73 LEAPVVVTGASRGIGATAGALGCKVLNVARSKEAEVEVSKEIEZASGGRAITFGG 132
| | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 8 LRQQAIVVTGASRGIGRAIALELANYGATVVNYASSSTADEVVAITGTGGEAVAKA 67
| | | | | | | | | | | | | | | | | | | | | : | | | | |

QY 133 DYSKEADVSMKAADLKGTTIPLVNNAGITRTDILLRMKKSQWQDVILNLTGTVFLCT 192
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
Db 68 DVSQEVEDNLINGAIDKFRIIDLIVNNAGITRTDILLRMKPEDWAVIDLNLTGTVFLCT 127
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |

QY 193 QAATKMVKRKGIINIASVGLTGVNGQANYSAKAGVIGFTKTAREVASRNINNA 252
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
Db 128 RAVSKMLQRSGRIINITSVACQMGPQQANYSAKAGVIGFTKTAKELASRGITVNA 187
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |

QY 253 IAPGFIASDMTABGLEBKLIISTIPLGRYGOPEEVAGLVFEFLANPAASYMTGQVLT 312
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
Db 188 VAPGFATDWTSLNSE--GIIQYLGRYGOPEEIRAGNVRFIAADPAAAYITGVFNV 244
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |

QY 313 DGGMVM 318
| | | | |
Db 245 DGGMMV 250
| | | | |

RESULT 7
CB3961
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saeki, R.; Masui, N.; Fujii, F.; Hi
Nucleic Acids Res. 28, 4317-4331, 2000
A;/title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans ar
A;/Reference number: AB3650; UID:20512582; PMID:11058132
A;/Accession: CB3961
A;/Status: preliminary
A;/Molecule type: DNA
A;/Residues: 1-246 <STO>
A;/Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06210.1; GSPDB:GN
A;/Experimental source: strain C-125
C;Genetics:
A;/Gene: fabg
C;/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 45.7%; Score 712.5; DB 2; Length 246;

Best Local Similarity 57.7%; Pred. NO. 2.9e-40;
Matches 142; Conservative 41; Mismatches 62; Indels 1; Gaps 1;
QY 73 LEAPVVVTGASRGIGKATATGALGAGCKVLVNYARSSKEAEVSKTEIASGGEAITFGG 132
D 2 LOGKTAIVTGAASRGIGRATATGALGAGCKVLVNYARSSKEAEVSKTEIASGGEAITFGG 61
QY 133 DVSKEADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRMKSSQWQVIDNLNLTGVFLCT 192
D 62 DVADSESQAMVXETIDTDFGAVDILVNNAGITRDLNFRMKEEDWDVADIDNLNLTGVFLCT 121
QY 193 QAAATKVMKKGKGIINIASVVLGTGNVGOANYSAAGVIGTGTVAREVYASRNINVA 252
D 122 KAVTRPMKQKSGRIINVSIVGAGNAGQANYVAKAGVIGTGTVAREVYASRNINVA 181
QY 253 IAPGFASDMTAEIGEELEKILSTPLGRYQGPPEVAGLVFELALNPAASVMTGVOLTI 312
D 182 VAPGFETDMTGELPEDVKAQMLGQIPLARLGQPEEVAKVRFLA-SDDASYLGTQTHV 240
QY 313 DGGVMV 318
D 241 NGGMV 246
RESULT 8
A69621
N:oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [validated] - Bacillus subtilis
A:Alternate names: 3-ketoacyl-acyl carrier protein reductase
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence revision 05-Dec-1997 #text_change 21-Jul-2000
C:Accession: A69621; PC4176; T46633
R:Kunst, F.; Ogasawara, N.; Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertez
C.; Bron, S.; Brouillet, N.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.F.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69621
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-246 <KUN>
A:Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13464.1; PID:g2633963
A:Experimental source: strain 168
R:Oguro, A.; Kakeshita, H.; Takamatsu, H.; Nakamura, K.; Yamane, K.
Gene 172, 17-24, 1996
A:Title: The effect of Srb, a homologue of the mammalian SRP receptor alpha-subunit, on
A:Reference number: JC4819; MUID:96257247; PMID:8654983
A:Accession: PC4176
A:Molecule type: DNA
A:Residues: 230-246 <OGU>
A:Cross-references: DBJ:D64116; NID:g1389548; PIDN:BA10974.1; PID:g1237012
R:Cronan, J.E.; Morbidoni, H.R.; de Mendoza, D.
J. Bacteriol. 178, 4794-4800, 1996
A:Title: Bacillus subtilis acyl carrier protein is encoded in a cluster of lipid biosynt
A:Reference number: Z23107; MUID:96326321; PMID:8759840
A:Accession: T46633
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22, 'A', 24-246 <CRO>
A:Cross-references: EMBL:U59433; NID:g1502418; PIDN:AA044307.1; PID:g1502421
A:Experimental source: strain 168
C:Genetics:
A:Gene: fabG; srb

A:Map position: 135-145 degrees
C:Function:
A:Description: EC 1.1.1.100 [validated, MUID:96326321]
A:Pathway: fatty acid biosynthesis
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: fatty acid biosynthesis; NADP; oxidoreductase
F:5-185/Domain: short-chain alcohol dehydrogenase homology <SADH>
F:154/Active site: Tyr #status predicted

Query Match 45.6%; Score 711.5; DB 2; Length 246;
Best Local Similarity 56.9%; Pred. No. 3.4e-40;
Matches 140; Conservative 47; Mismatches 58; Indels 1; Gaps 1;
QY 73 LEAPVVVTGASRGIGKATATGALGAGCKVLVNYARSSKEAEVSKTEIASGGEAITFGG 132
D 2 LOGKTAIVTGAASRGIGRATATGALGAGCKVLVNYARSSKEAEVSKTEIASGGEAITFGG 61

QY 133 DVSKEADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRMKSSQWQVIDNLNLTGVFLCT 192
D 62 DVSNPEDVQNMKIKETLSVFSTIDILVNNAGITRDLNLMRMKDEDDVDVINLKGVENCT 121
QY 193 QAAATKVMKKGKGIINIASVVLGTGNVGOANYSAAGVIGTGTVAREVYASRNINVA 252
D 122 KAVTRPMKQKSGRIINVSIVGAGNAGQANYVAKAGVIGTGTVAREVYASRNINVA 181
QY 253 IAPGFASDMTAEIGEELEKILSTPLGRYQGPPEVAGLVFELALNPAASVMTGVOLTI 312
D 182 IAPGFISTDMTDLAKDVQDEMLQIPLARFGSPDSVSVVTFIA-SEGARYMTGQTLHI 240
QY 313 DGGVMV 318
D 241 DGGVMV 246

RESULT 9

AG1300
3-ketoacyl-acyl carrier protein reductase homolog fabG [imported] - Listeria monocytog
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AG1300
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloech
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlar
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1300
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99885.1; PID:g16411261; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: fabG

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 44.0%; Score 686.5; DB 2; Length 247;
Best Local Similarity 55.3%; Pred. No. 1.5e-38;
Matches 136; Conservative 42; Mismatches 67; Indels 1; Gaps 1;
QY 73 LEAPVVVTGASRGIGKATATGALGAGCKVLVNYARSSKEAEVSKTEIASGGEAITFGG 132
D 3 LOGKVAVVTGSGRGIGRDIAINLAKGANIFFNYNGSPAAEETAKLVAEHGVEVEMKA 62

QY 133 DVSKEADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRMKSSQWQVIDNLNLTGVFLCT 192
D 63 NVIAEDVDVAFQAIERFGRVDILVNNAGITRDLNLMRMKDEDDVDVINLKGFLCT 122
QY 193 QAAATKVMKKGKGIINIASVVLGTGNVGOANYSAAGVIGTGTVAREVYASRNINVA 252
D 123 KAVSRITMQRAGKIINMASVWGLIGNAGQANYVASKAGVIGTGTVAREVYASRNINVA 182

A;Residues: 1-249 <KUR>
A;Cross-references: GB:AB001437; PIDN:AAK81497.1; PID:g15026670; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3574
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

	Query Match	Best Local Similarity	Matches	Score	DB 2;	Length	Indels	Gaps
QY	73	LEAPVVVVTGASRGICKATALGKAGCKVLVNVARSSKEAEBSVEISGEAITFGG	132	42.9%;	Score 669.5;	DB 2;	Length 249;	
Db	5	LSGKVAVVTGAGRLGRAIALKAEGANLVNVRSSSEAEOKLKEIEELSGKAVAKA	64	52.8%;	Pred. No. 2.1e-37;			
QY	133	DVSKEADVESMMKAALDKWGTIDVLVNNAGITRDTLLMEMKKSQWDVIDNLNTGVFLCT	192	Conservative 50;	Mismatches 65;			
Db	65	DISKYDEATIINKALDEGTVDILVNNAGITRDNLMLMKKEEDFDSVINVLKGAFNCI	124					
QY	193	QAATKVMKKRKGIINIASVVGLTGNVGQANYSAAGVIGFTKTVAREYASRNINNA	252					
Db	125	KHTRSVMLKCKSKIINISSVGLIGNAQGVNYAAKAGIIGMTXSVAKELASRGITVNA	184					
QY	253	IARGFTASDMTAEELGEEKKILSTPIGRYGQPEHVAGLVFEFLALNPAAASYMTGOVLTT	312					
Db	185	VAPGIITSMDTALTDRKESIVAAVPLNKVGEADVANLVFLA-SDLSSYYITGQVINV	243					
QY	313	DGGWMV 318						
Db	244	DGGWMV 249						

RESULT 12
B89896
3-oxoacyl-(acyl-carrier protein) reductase [imported] - Staphylococcus aureus (s)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: B89896
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimi, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: B89896
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-246 <KUR>
A;Cross-references: GB:BA000018; PID:g13701031; PIDN:BAB42326.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: fabG
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

	Query Match	Best Local Similarity	Matches	Score	DB 2;	Length	Indels	Gaps
QY	79	VVTGASRGICKATALGKAGCKVLVNVARSKRAEBSVEISGEAITFGGDVSKEA	138	42.2%;	Score 658.5;	DB 2;	Length 246;	
Db	8	LVTGASRGIGRSIALQLAAEEGYNVNNAVGSKEAEAVVEEIKAKGVDSFAIQVANADAD	67	55.0%;	Pred. No. 1.1e-36;			
QY	139	DVSNMKAALDKWGTIDVLVNNAGITRDTLLMEMKKSQWDVIDNLNTGVFLCTQAARKV	198	Conservative 44;	Mismatches 63;			
Db	68	EYVKMIKEVVSFGSLDVLVNNAGITRDNLMLMKKEQEWDVIDTNLRGXVFNCIOKATPQ	127					
QY	199	MMKKKGIINIASVVGLTGNVGQANYSAAGVIGFTKTVAREYASRNINNAIPAGFI	258					
Db	128	MLQRSGALINLSSVVGAVGPGQANYVTRAGVLGLTKSARELIASRGITTVNAVAPGI	187					
QY	259	ASDMTAELGEEKKILSTPIGRYGQPEEVAGLVFEFLALNPAAASYMTGOVLTTDGGWMV	318					
Db	188	VSDMTDALSDLKEOMLOTPILARFGDDTDANTVAFIA-SDKAYITGOTHWNGGMV	246					

```
RESULT 13
G75333
3-oxoacyl-acyl carrier protein reductase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: G75333
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75333
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <WHI>
A;Cross-references: GB:AE002033; GB:AE000513; NID:g6459726; PIDN:AAF11496.1; PID:g645973
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRI943
A;Map position: 1
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 41.0%; Score 639.5; DB 2; Length 254;
Best Local Similarity 52.9%; Pred. No. 2.1e-35;
Matches 128; Conservative 43; Mismatches 70; Indels 1; Gaps 1;

QY 75 APVVVVTGASRGIGKATALGKAGCKVLVNYARSSKEAEVSKIEASGGEAITFGDV 134
Db 11 ARVALVTGSRGGLGRVALRLAQDPTVAVHYGGEBAQOQVADIRAGGAQVFGADL 70

QY 135 SKRADVSMKKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWQDVLDNLGTGVFLCTQA 194
Db 71 SQPANAGTLEDVIAALGRDLVLVNNAGITRDTGLAIRMKQEDMDVQLTNLSFAACRA 130

QY 195 ATKVMKKKRGKIINIASVVLGTGNVGOANYSAKAGVIGFTKTVAREYASRNINVAIA 254
Db 131 ALKHMKNRSGRIYVNVSSVALAGNPGQAVYASKAGLIGLTRALAKYGGRGITVNAIA 190

QY 255 PGFIASDWTAEELGEEKILSTPLGRYGQPEVAGLVEFLALNPAASYMTGQVLTDG 314
Db 191 PGFTESDWTAKLPDXTKKQYQANIPLAFPGQPEVALVAFLA-SEGAGVITGQITGVDG 249

QY 315 GM 316
Db 250 GM 251

RESULT 14
F82128
3-oxoacyl- (acyl-carrier-protein) reductase VC2021 [imported] - Vibrio cholerae (strain N
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: F82128
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: F82128
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <HEI>
A;Cross-references: GB:AB004276; GB:AE003852; NID:g9656555; PIDN:AAF95169.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2021
A;Map position: 1
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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Query Match 39.8%; Score 621.5; DB 2; Length 248;
Best Local Similarity 51.4%; Pred. No. 3.2e-34;
Matches 127; Conservative 46; Mismatches 67; Indels 7; Gaps 4;

QY 73 LEAPVVVVTGASRGIGKATALGKAGCKVLVNYARSSKEAEVSKIEBASG-GEAITFG 131
Db 7 LEKQVALVTGASRGIGKATAEALAEAGKV-IGTATSESGAQAIISDYLGDNGKGMAL--- 62

QY 132 GDVSKADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWQDVLDNLGTGVFLC 191
Db 63 -NVTNPESIEAVLKAITDFGGVDILVNNAGITRDNLLARMKEEESWDINETNLTISFRL 121

QY 192 TQATATVMMKKRGKIINIASVVLGTGNVGOANYSAKAGVIGFTKTVAREYASRNINVN 251
Db 122 SKAVLRGMKKRGRIINVSVVGTGNAGQANYAAKAGVIGFTKSMAREVASRGVTVN 181

QY 252 AIAPGFIASDWTAEELGEEKILSTPLGRYGQPEVAGLVEFLALNPAASYMTGQVLIT 311
Db 182 TVAPGFIEDWTAKALNDQRTATLAQVPAGRLGDPREIASAVAFLA-SPEAAVITGETLH 240

QY 312 IDGGMVM 318
Db 241 VNGGMVM 247

RESULT 15
F86721
hypothetical protein fabG1 [imported] - Lactococcus lactis subsp. lactis (strain IL14C
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: F86721
R;Bolotin, A.; Wincker, P.; Mauer, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehr
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: F86721
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-243 <STO>
A;Cross-references: GB:AB005176; PID:g12723693; PIDN:AAK04872.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: fabG1
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 39.3%; Score 612.5; DB 2; Length 243;
Best Local Similarity 51.5%; Pred. No. 1.2e-33;
Matches 124; Conservative 44; Mismatches 68; Indels 5; Gaps 2;

QY 78 VVVTGASRGIGKATALGKAGCKVLVNYARSSKEAEVSKIEASGGEAITFGDVSK 137
Db 8 VFTVGTGRIGKAIALQFAKAGSNLIIN--GRSAISEELAEFTAYGVKAVGISGDISKS 65

QY 138 ADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWQDVLDNLGTGVFLCTQAATK 197
Db 66 EDKQVVAEAIETLSGVDILVNNAGITRDTGLSLKMSSEDPESVLKINLTGAFNMTQAVLK 125

QY 198 VMKKKRGKIINIASVVLGTGNVGOANYSAKAGVIGFTKTVAREYASRNINVAIAPGF 257
Db 126 PMTRARSAGIINISVVVLGMENAGQANYAASKAGLIGLTRKSIAREVAARVVRVNAVAPGF 185

QY 258 IASDWTAEELGEEKILSTPLGRYGQPEVAGLVEFLALNPAASYMTGQVLTDGMV 317
Db 186 IESDWTAEVLSKVDKADWKQIEMKRFMPMEIATATQFLA---EQEYMTGQVLTDGGSV 242

QY 318 M 318
Db 243 M 243

Search completed: November 7, 2003, 21:04:59
Job time : 27 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 19:34:11 ; Search time 17 Seconds
(without alignments)
879.676 Million cell updates/sec

Title: US-10-024-806-2
Perfect score: 1560
Sequence: 1 MATAAATAAAAVSPAAAG.....NPAASYMTGVLTIDGGWM 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1130	72.4	320	1	FABG_CUPLA
2	1039.5	66.6	319	1	FABG_ARATH
3	800.5	51.3	247	1	FAGI_SYNY3
4	711.5	45.6	246	1	FABG_BACSU
5	692.5	44.4	201	1	FABG_BRANA
6	621.5	39.8	244	1	FABG_VTECH
7	592	37.9	246	1	FABG_THEMA
8	584.5	37.5	244	1	FABG_VTECH
9	576.5	37.0	244	1	FABG_ECOLI
10	575.5	36.9	248	1	FABG_AQUAE
11	574.5	36.8	244	1	FABG_SALTY
12	556	35.6	247	1	FABG_PSEAE
13	545.5	35.0	242	1	FABG_HABIN
14	542.5	34.8	248	1	FABG_CHLMU
15	532.5	34.1	247	1	FABG_CHLTP
16	528	33.8	248	1	FABG_CHLTP
17	508.5	32.6	241	1	FABG_RICPR
18	499.5	32.0	245	1	NODG_RHS3
19	488.5	31.3	246	1	NODG_AZOB
20	487.5	31.2	241	1	PHBB_ZOORA
21	473	30.3	261	1	DHG2_BACME
22	471.5	30.2	244	1	FABG_BUCAP
23	468.5	30.0	241	1	PHBB_RHIME
24	464.5	29.8	244	1	FABG_BUCAI
25	464	29.7	246	1	PHBB_CHRVI
26	463	29.7	261	1	DHGA_BACME
27	459.5	29.5	247	1	YD50_MYCTU
28	459	29.4	261	1	DHG3_BACME
29	457	29.3	261	1	DHGA_BACME
30	456.5	29.3	258	1	DHG2_BACSU
31	455.5	29.2	245	1	NODG_RHIME
32	454	29.1	245	1	FABG_BUCBP
33	451	28.9	261	1	DHG_BACSU

34	448.5	28.7	253	1	KDUD_ECOLI
35	447	28.7	248	1	PHAB_ACISP
36	444	28.5	261	1	DHGI_BACME
37	443.5	28.4	255	1	FABG_MYCSM
38	443	28.4	261	1	DHG_BACWE
39	442.5	28.4	240	1	FAG2_SYNY3
40	439.5	28.2	247	1	FABG_MYCTU
41	434.5	27.9	242	1	PHAB_PARDE
42	426.5	27.3	246	1	PHBB_ALCEU
43	425.5	27.3	261	1	ACT3_STRCO
44	423.5	27.1	261	1	DHB8_HUMAN
45	423.5	27.1	262	1	DHGB_BACME

ALIGNMENTS

RESULT 1

FABG_CUPLA

ID_FABG_CUPLA STANDARD; PRT; 320 AA.

AC F28643;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor
DE (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
GN CLKR27.
OS Cuphea lanceolata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Cuphea.
OX NCBI_TaxID=3930;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92293104; PubMed=1376402;
RA Klein B., Pawlowski K., Hoerike-Grandpierre C., Schell J.,
RA Toepfer R.;
RT "Isolation and characterization of a cDNA from Cuphea lanceolata
encoding a beta-ketoacyl-ACP reductase.";
RL Mol. Gen. Genet. 233:122-128(1992).
CC -! CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH
CC -! PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -! SUBUNIT: Homotetramer (Probable).
CC -! SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
PLASTIDS.
CC -! SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.

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EMBL; X64566; CAA45866.1; -.
PIR; S22450; S22450.
DR HSSP; P50162; 1AE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 62 320 3-OXOACYL-[ACYL-CARRIER PROTEIN]
FT NP_BIND 82 106 REDUCTASE.
FT ACT_SITE 227 227 NADP (BY SIMILARITY).
FT BY_SIMILARITY 227 227 BY SIMILARITY.
SQ SEQUENCE 320 AA; 33103 MW; 06BAF0522B2B8C87 CRC64;

Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

-!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.

-!- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.

-!- SUBUNIT: Homotetramer (Probable).

4 AAATTAATAAVSSPAARGAAGAAASRRGFTVTCGGGAARFSP-TIRSGRFSG--VQTHVA 60
||||| : ||| : ||| : ||| : ||| :
2 AAAVAAPRLISLKAVAKLGFREISOQLAPLHSAIPHFGMLRCRGRPFSTSWKRAQT 61

RA	Willschneider J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,	
RA	Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,	QY
RA	Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,	
RA	Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,	DB


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QY 61 AVEQAVVVDATKLEAPVVTGASRGIGKATALAGKAGCKVLNVYARSSKEAEVSKEI 120
Db 62 ATQSPGEVQVQKESPVVVTGASRGIGKATALAGKAGCKVLNVYARSSKEAEVAKQI 121
QY 121 EASGGEAITFGDVSKEADYEMMKAALDKWGTIDVLVNNAGITRDTLLMRMKKSQWDV 180
Db 122 EYGGQAITFGDVSKEADYEMMKAALDKWGTIDVLVNNAGITRDTLLMRMKKSQWDEV 181
QY 181 IDNLNLTGTVFVCTQAAATKVMKKRKGKLIINTASVVLGTGNVGOANYSAAGVIGFTKTIVA 240
Db 182 IALNLTGTVFVCTQAAATKVMKKRKGKLIINTASVVLGTGNVGOANYSAAGVIGFTKTIVA 241
QY 241 REVASRNINNVNAPGFIASDMTAEELGEEKILSTIPLGRYGOPEEVAGLVEFLALNP 300
Db 242 REGASRNINNVNAPGFIASDMTAEELGEEKILSTIPLGRYGOPEEVAGLVEFLALNP 301
QY 301 AASYITGQVLTIDGGMV 318
Db 302 AASYITGQVLTIDGGMV 319

```

RESULT 3

```

FAGI_SYN3
ID FAGI_SYN3 STANDARD; PRT; 247 AA.
AC P73574;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase 1 (BC 1.1.1.100) (3-
DE ketoacyl-acyl carrier protein reductase 1).
DE FAGI OR SLR0886.
GN Synechocystis sp. (strain PCC 6803).
OS Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiuwa M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada A., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -!- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D90907; BAA17614.1; -
CC DR PIR; S77280; S77280.
CC DR HSSP; P50162; IAE1.
CC DR InterPro; IPR002198; ADH_short.
CC DR Pfam; PF00106; adh_short; 1.
CC DR PRINTS; PR00080; SDRFAMILY.
CC DR PROSITE; PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 11 35 NADP (BY SIMILARITY).
FT ACT_SITE 156 156 BY SIMILARITY.
SQ SEQUENCE 247 AA; 25724 MW; 91EBF9409C777E20 CRC64;

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Query Match 51.3%; Score 800.5; DB 1; Length 247;
Best Local Similarity 65.3%; Pred. No. 4.7e-44;
Matches 162; Conservative 30; Mismatches 53; Indels 3; Gaps 1;
QY 71 TKLEAPVVTGASRGIGKATALAGKAGCKVLNVYARSSKEAEVSKETASGEAITF 130
Db 2 TALTAQVALVTGASRGIGKATALAGKAGCKVLNVYARSSKEAEVSKETASGEAIAV 61
QY 131 GGDVSKEADYEMMKAALDKWGTIDVLVNNAGITRDTLLMRMKKSQWDVIDLNLGTGVL 190
Db 62 QANVANADEVDQIKTKTLDFKSRIDVLVNNAGITRDTLLMRMKLEDQWQAVIDLNLGTGVL 121
QY 191 CTQAAATKVMKKRKGKLIINTASVVLGTGNVGOANYSAAGVIGFTKTIVAREVASRNIN 250
Db 122 CTKAVSKMLKQKSGRIINTSVAGMMGNPGQANYSAAGVIGFTKTIVAKELASRGVT 181
QY 251 NAIAPGFASDMTAEELGEEKILSTIPLGRYGOPEEVAGLVEFLALNPAAASYITGQVLT 310
Db 182 NAVAPOFIATDMTNLNAE---PILOFIPLARYGOPEEVAGIRFLATDPAAAYITGQTF 238
QY 311 TIDGGMV 318
Db 239 NVDGGMV 246

```

RESULT 4

```

FAGI_BACSU
ID FAGI_BACSU STANDARD; PRT; 246 AA.
AC P51831; O31733;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (BC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
DE FAGI.
GN Bacillus subtilis.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96326321; PubMed=8759840;
RA Morbidoni H.R., de Mendoza D., Cronan J.E. Jr.;
RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of
RT lipid biosynthesis genes.";
RL J. Bacteriol. 178:4794-4800(1996).
CC [2]
CC SEQUENCE FROM N.A.
CC STRAIN=168;
CC MEDLINE=98044033; PubMed=9384377;
CC RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
CC Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
CC Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
CC Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
CC Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
CC Entian K.D., Ewing J., Fabret C., Ferrari E., Foulger D.,
CC Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
CC Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
CC Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
CC Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
CC Joris B., Karamata D., Kishimoto Y., Kishimoto Y., Kishimoto Y.,
CC Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
CC Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
CC Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
CC Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
CC Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
CC Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
CC Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
CC Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
CC Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
CC Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

```

RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Togmon A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzneger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*.";
 RL Nature 390:249-256 (1997).
 RN [3]
 RP SEQUENCE OF 1-172 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98195738; PubMed=9534248;
 RA Foulger D., Errington J.;
 RT "A 28 kbp segment from the spvM region of the *Bacillus subtilis* 168
 RL genome.";
 RN Microbiology 144:801-805 (1998).
 RP [4]
 RP SEQUENCE OF 230-246 FROM N.A.
 RC STRAIN=168;
 RA Oguro A., Kakeshita H., Takamatsu H., Nakamura K., Yamane K.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
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 CC -----
 DR EMBL; U59433; AAC4307.1; -;
 DR EMBL; Z99112; CAB13464.1; -;
 DR EMBL; Y13937; CAA74250.1; -;
 DR EMBL; D64116; BAA10974.1; -;
 DR PIR; A69621; A69621.
 DR HSP; Q12634; 1YBV.
 DR Subtilist; BG11535; fabg.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; FALSE NEG.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 9 33
 FT ACT_SITE 154 154
 FT CONFLICT 23 23
 FT SEQUENCE 246 AA; 26282 MW; C6A391167D3237DC CRC64;
 Query Match 45.6%; Score 711.5; DB 1; Length 246;
 Best Local Similarity 56.9%; Pred. No. 2e-38;
 Matches 140; Conservative 47; Mismatches 58; Indels 1; Gaps 1;
 QY 73 LEAPVVVVTGASRGIGKATLALGACGKVLVNYARSKAEVSKFIRASGGEAITFGG 132
 DB 2 LNDKTAIVTGSRGIGRSIALDLAKSGANVYVYSGNEAKANEVVDSEIKSGKAIIVKA 61
 QY 133 DVSKAEAVESNMKALDKNGTIDVIVNAGITRITLIRMKKQSQVQVIDNLITGVFLCT 192
 DB 62 DVSNFEDVQNMKEKTLVSFSTIDILVNAGITRNLIRMKDEMDVDVINILKGVNCT 121
 QY 193 QATKVMKRGKIIINIASVVGITGNVGOANYSAAGVIGFTKTVAREVYASNNIVNA 252
 DB 122 XAVTRQMKQKSGRIINVSIVGVSGNPGQANYVAAKAGVIGLTKSSAKELASNIIVNA 181
 QY 253 IAPGFASDMTAELEGELEKILSTIPLRGYQGPPEVAGLVFLALNPAASVYMTGVQLTI 312
 DB 182 IAPGFISTDNTDKLADVQDEMLKQIPLARFGPEPSVSVVTFILA-SEGARYMTGQTLHI 240
 QY 313 DGGNVM 318

DB 241 DGGNVM 246
 RESULT 5
 ID FABG_BRANA STANDARD; PRT; 201 AA.
 AC P27582;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase [EC 1.1.1.100] (3-ketoacyl-
 DE acyl carrier protein reductase) (Fragments).
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE OF 35-62 AND 81-84.
 RC TISSUE=Seed;
 RX MEDLINE=92223071; PubMed=1562581;
 RA Sheldon P.S., Kekwick R.G.O., Smith C.G., Sidebottom C.M.,
 RA Slabas A.R.;
 RT "3-oxoacyl-[ACP] reductase from oilseed rape (*Brassica napus*).";
 RL Biochim. Biophys. Acta 1120:151-159 (1992).
 RN [2]
 RP SEQUENCE OF 63-201 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=92246853; PubMed=1575676;
 RA Slabas A.R., Chase D., Nishida I., Murata N., Sidebottom C.,
 RA Safford R., Kekwick R.G., Sheldon P.S., Hardie D.G., Mackintosh R.W.;
 RT "Molecular cloning of higher-plant 3-oxoacyl-[acyl carrier protein]
 RT reductase. Sequence identities with the nodG-gene product of the
 RT nitrogen-fixing soil bacterium *Rhizobium meliloti*.";
 RL Biochem. J. 283:321-326 (1992).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
 CC -1- SUBUNIT: Homotetramer (Probable).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
 CC PLASTIDS.
 CC -1- TISSUE SPECIFICITY: EMBRYO AND LEAF TISSUES.
 CC -1- MISCELLANEOUS: EXHIBITS A MARKED PREFERENCE FOR ACYL-CARRIER
 CC PROTEIN DERIVATIVES OVER COA DERIVATIVES AS SUBSTRATES.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -----
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 CC -----
 DR EMBL; X64463; CAA45793.1; -;
 DR PIR; S22417; S22417.
 DR HSP; P50162; 1AE1.
 DR InterPro; IPR002198; ADH_short.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast.
 FT NON_CONS 27 28
 FT NON_CONS 34 35
 FT NON_CONS 62 63
 FT ACT_SITE 108 108 BY SIMILARITY.
 SQ SEQUENCE 201 AA; 21042 MW; FD51B2E369D2D967 CRC64;
 Query Match 44.4%; Score 692.5; DB 1; Length 201;
 Best Local Similarity 57.8%; Pred. No. 2.5e-37;
 Matches 149; Conservative 23; Mismatches 27; Indels 59; Gaps 3;

Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
[4]
SEQUENCE FROM N.A.
SPECIES=6.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
Yu J.;
"Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
through comparison with genomes of *Escherichia coli* K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.

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EMBL; M84991; AAA23739.1; -.
EMBL; AE000210; AAC74177.1; -.
EMBL; D90745; BAA35901.1; -.
EMBL; AE015136; AAN42716.1; -.
PIR; B64853; B42147.
PDB; 1I01; 21-DEC-01.
EcGene; EG11318; fabG.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome;
3D-structure.
FT NP_BIND 10 34 NADP (BY SIMILARITY).
FT ACT_SITE 151 151 BY SIMILARITY.
FT CONFLICT 30 30 A -> G (IN REF. 1).
FT SEQUENCE 244 AA; 25560 MW; 48EC1F2A77EEFD9 CRC64;
Query Match 37.0%; Score 576.5; DB 1; Length 244;
Best Local Similarity 49.4%; Pred. No. 6.7e-30;
Matches 121; Conservative 45; Mismatches 74; Indels 5; Gaps 3;
QY 74 EAPVVVVTGASRGIGKATALGKAGKVLVNYARSSKEAEVSKVEITGGD 133
DB 4 EGKIALVTGASRGIGKATALGKAGKVLVNYARSSKEAEVSKVEITGGD 59
QY 134 VSKEADVSMKAAALDKWGTIDVLVNNAGITDITLLMRKKSQMDVIDNLITGVFLCTQ 193
DB 60 VTPDASIESVLEKIRAEFEVDILVNNAGITDITLLMRKKSQMDVIDNLITGVFLSK 119
QY 194 AATKVMKKRKGKINIASVGLTGNVGOANYSAAGVIGFTKTVAEYASRNINVAI 253
DB 120 AVNRAMKKRRHRIITIGSVGTGNGGQANYAAKAGLIGFSKLAEVARGITNVV 179
QY 254 ACGFIASDWTAELEGELEKILSTPLGRYGOPEVAGLVEFLALNPAASITQVLTID 313
DB 180 AFGFIETDTRALSDQDAGILAQVPAAGLGAQBIANAVAFASDEAA-YITGETLHV 238
QY 314 GGMVM 318
DB 239 GGMVM 243

SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PA01;
MEDLINE=99193062; PubMed=10464226;
Kutchma A.J., Hoang T.T., Schweizer H.P.;
"Characterization of a *Pseudomonas aeruginosa* fatty acid biosynthetic
gene cluster: purification of acyl carrier protein (ACP) and malonyl-
coenzyme A:ACP transacylase (fabD).";
J. Bacteriol. 181:5498-5504 (1999).
[2]
SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PA01;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Young
[1]

4


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SEQUENCE FROM N.A.
RP STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Keiley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
RR -!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC
CC -!- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U32701; AAC21824.1; -.
DR PIR; D64051; D64051.
DR DR HSSP; PI9992; LHDC.
DR TIGR; HI0155; -.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
KW NP BIND 8 32 NADP (BY SIMILARITY).
FT ACT SITE 149 149 BY SIMILARITY.
SQ SEQUENCE 242 AA; 25507 MW; B3DE2E2C020D2F71 CRC64;

Query Match 35.0%; Score 545.5; DB 1; Length 242;
Best Local Similarity 46.3%; Pred. No. 6e-28;
Matches 114; Conservative 51; Mismatches 76; Indels 5; Gaps 3;

QY 73 LEAPVVVTGASRGIGKATALAGKAGCKVLVNTYARSSEKEAEYSKEIEASGEAITFGG 132
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|
1 MQGKIALVTGTRGLGRALAEELSKGAFV-IQTATSEKGAEIASAYLGDKGKGLVL--- 56

QY 133 DVSREADVESMMKAALDKWGTIDVLVNNAGITRTDTLLMRMKKSQWDVIDLNLTGVFLLCT 192
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|
57 NVTDKESIETLEIQIKNDPGFDIDILVNNAGITRDNLLNRKDEEWFDDMQNLTSTVYHLS 116

QY 193 QAATKVMKKRKGIININTASVVGITGNVGQANYSAAKAGVTFPTKTVAEYASRNINVNA 252
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|
117 KAMLRSMKKRFGRINIINGSVSGTGNPGQNYCAAKAGVGVGFSEKLAKAWEAAARGITVNV 176

QY 253 IAPGFIAIDMTAEIAGEELEKKILTIPLGRYGOPEEVAGLYFEFLALNPAAASYMTQVLTII 312
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|
177 VAPGFIAIDMTTEVLTVDEQGILSNVPAGRLGEAKDIKAVAFLA-SDDAGYITTTTLHV 235

QY 313 DGGMYM 318
DB :|::|
236 NGGLYL 241

RESULT 14
IID_FABG_CHLMU STANDARD; PRT; 248 AA.
AC Q9PF7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
```

```

16-OCT-2001 (Rel. 40, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
acyl carrier protein reductase).
FABG OR TC0508.
Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Mi99;
RX MEDLINE=90000809; PubMed=10694935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heideberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Barry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT 'Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.';
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -|- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -|- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -|- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
-----
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or send an email to license@isb-sib.ch).
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EMBL: AE002319; AAP39350.1; -.
PIR: E81695; E81695.
HSSP: P50163; 2AE1.
TIGR: TC0508; -.
InterPro: IPR002198; ADH_SHORT; 1.
Pfam: PF00106; adh_short; 1.
PRINTS: PR00080; SDRFAMILY.
PROSITE: PS00061; ADH_SHORT; 1.
Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT NP BIND 12 36 NADP (BY SIMILARITY).
FT ACT SITE 157 157 BY SIMILARITY.
SQ SEQUENCE 248 AA; 25977 MW; 1F5C8968CB05FF58 CRC64;

Query Match 34.8%; Score 542.5; DB 1; Length 248;
Best Local Similarity 46.9%; Pred. No. 9.6e-28;
Matches 112; Conservative 47; Mismatches 77; Indels 3; Gaps 3;

QY 79 VVTGASRGIGKATLALGKAGCKVLVNYARSSKEAEVSEIEASGGEAITFG-GDVSKE 137
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
11 IVTGGSGIGFGIAGLFAEAGANVQI-WGNEEAGSAQAODLSKDTGSKVSFALVDVSKN 69
QY 138 ADVESMMKKAALDKWTIDVLVNNAGITRDTLLMRKKSQWQVDIDLNLTVGFLCTQAATK 197
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70 DMVSAQVQKFLAEGYIDVNNAGITRDSLLMRMSEEESSVIDINLGSIVNVCSAVIR 129
QY 198 VMKKRKGKIIINIASVGLTGNVQANYSAAGVGITKTIVAREVASNNINVAIPGF 257
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
130 PMTKARSGAIVNISSIVGLRSGPQNTNAAAGIIGFSKALSKVSGKNIRVNCIAPGF 189
QY 258 IASDMTAEELGEELEKILSTIPLGRYGOPEEAGLVFEFLALNPAASVMTGQVLTIDGGM 316
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
190 IDTDMTKGLSDNLKNEWLKGVPLGRVGTPEEIAAALFLASN-QSSYITGQVLSVDGGM 247

RESULT 15
FABG_CHLTR
ID FABG_CHLTR STANDARD; PRT; 247 AA.
AC F38004; O84240;
DT 01-OCT-1994 (Rel. 30, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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16-OCT-2001 (Rel. 40, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
acyl carrier protein reductase).
FABG OR CT237.
Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/CX;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.D., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT 'Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.';
RL Science 282:754-759(1998).
RN [2]
RP SEQUENCE OF 1-10 FROM N.A.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christensen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -|- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -|- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -|- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
-----
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-----
EMBL: AE001297; AAC67830.1; -.
PIR: F71538; F71538.
HSSP: P47227; 1BDB.
DR Siena-2DPAGE; P38004; -.
DR InterPro: IPR002198; ADH_SHORT.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT INIT MET 0 0
FT NP BIND 11 35 NADP (BY SIMILARITY).
FT ACT SITE 156 156 BY SIMILARITY.
FT CONFLICT 2 2 G -> T (IN REF. 2).
SQ SEQUENCE 247 AA; 25888 MW; F98A1F17264F4EC1 CRC64;

Query Match 34.1%; Score 532.5; DB 1; Length 247;
Best Local Similarity 46.0%; Pred. No. 4.1e-27;
Matches 110; Conservative 47; Mismatches 79; Indels 3; Gaps 3;

QY 79 VVTGASRGIGKATLALGKAGCKVLVNYARSSKEAEVSEIEASGGEAITFG-GDVSKE 137
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
10 IVTGGSGIGFGIAGLFAEAGANVQI-WGNEEAGSAQAQTLSEQTGRQVSPALVDVSKN 68
QY 138 ADVESMMKKAALDKWTIDVLVNNAGITRDTLLMRKKSQWQVDIDLNLTVGFLCTQAATK 197
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
69 DMVSAQVQKFLAEGYIDVNNAGITRDSLLMRMSEEESSVIDINLGSIVNVCSAVIR 128
QY 198 VMKKRKGKIIINIASVGLTGNVQANYSAAGVGITKTIVAREVASNNINVAIPGF 257
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
129 PMTKARSGAIVNISSIVGLRSGPQNTNAAAGIIGFSKALSKVSGKNIRVNCIAPGF 188
QY 258 IASDMTAEELGEELEKILSTIPLGRYGOPEEAGLVFEFLALNPAASVMTGQVLTIDGGM 316
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
189 IDTDMTKGLSDNLKNEWLKGVPLGRVGTPEEIAAALFLA-SDGSYITGQVLSVDGGM 246

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Search completed: November 7, 2003, 21:03:19
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: November 7, 2003, 20:49:21 ; Search time 60 Seconds
(without alignments)
1367.679 Million cell updates/sec

Title: US-10-024-806-2
Perfect score: 1560
Sequence: 1 MATAAATAAAVSSPAARG.....NPASVMTGQVLTIDGGVMV 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_unclassified:*
14: sp_vertebrate:*
15: sp_xvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1093	70.1	315	10	Q949M3
2	1093	70.1	320	10	Q93X62
3	1078.5	69.1	328	10	Q93X67
4	1068	68.5	317	10	Q93X68
5	1040.5	66.7	254	10	Q949M2
6	794.5	50.9	251	16	Q8YV70
7	777.5	49.8	245	16	Q8DLS9
8	712.5	45.7	246	16	Q9KA03
9	701.5	45.0	246	16	Q8ER07
10	700.5	44.9	257	2	Q8GE35
11	686.5	44.0	247	16	Q8Y690
12	681.5	43.7	247	16	Q92AK1
13	674.5	43.2	247	16	Q8R9W0
14	669.5	42.9	249	16	Q97DA6
15	659.5	42.3	246	16	Q8X1H1
16	658.5	42.2	246	16	Q99QK7

17	647.5	41.5	244	16	Q8CPI3
18	639.5	41.0	254	16	Q9RT26
19	626	40.1	254	16	Q8EXX5
20	619	39.7	301	5	Q8I2S7
21	614	39.4	301	5	Q965D6
22	612.5	39.3	243	16	Q9CHP7
23	611.5	39.2	248	16	Q8D8G8
24	597.5	38.3	243	16	Q8DRI5
25	596.5	38.2	243	16	Q9FBC3
26	595.5	38.2	244	16	Q8ZNN2
27	595.5	38.2	244	16	Q8K628
28	591	37.9	245	16	Q8KAP0
29	590.5	37.9	248	16	Q8EDH3
30	587.5	37.7	244	16	Q99YD6
31	580.5	37.2	244	16	Q8E723
32	580.5	37.2	244	16	Q8E1K6
33	576	36.9	247	16	Q8PB09
34	573.5	36.8	244	16	Q8X3I5
35	571	36.6	247	16	Q9PFI6
36	567	36.3	247	16	Q8PNE4
37	559	35.8	248	16	Q9JXR1
38	559	35.8	248	16	Q9JW61
39	558.5	35.8	244	16	Q8ZFT5
40	558.5	35.8	244	16	Q8DSN5
41	554	35.5	247	2	Q8GI82
42	549	35.2	249	16	Q8Y0J2
43	545.5	35.0	247	16	Q9PI70
44	544.5	34.9	242	16	Q9CJS6
45	537.5	34.5	244	2	Q9RA33

ALIGNMENTS

RESULT 1

Q949M3 PRELIMINARY; PRT; 315 AA.
AC Q949M3, 2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE 3-oxacyl-[acyl carrier protein] reductase (EC 1.1.1.100).
GN BKE3
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
CX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RA McDonald F.S., White A.J., Elborough K.M., Slabas A.R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
DR EMBL: AJ243085; CAC41364.1; -;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 315 AA; 33140 MW; 3B0B36C94A4FB313 CRC64;

Query Match 70.1%; Score 1093; DB 10; Length 315;
Best Local Similarity 80.7%; Pred. No. 2.3e-56;
Matches 213; Conservative 28; Mismatches 23; Indels 0; Gaps 0;

QY	55	VQTHAAVQAVVVDATKLEAPVVVTGASRGTKATALGAGCKLVNYSARSKAE	114
Db	52	VKAQATAVGEATGPEVPKVESPVVVVTGASRGIGKATLALGAGCKLVNYSARSKAE	111
QY	115	EVSKEITEASGEAITGGDVSKEDVSNKALDKWGTIDVLNNAGITRDITLLRMKK	174
Db	112	EVSQKIEAGGQAITFGGDVSKEDVSNKALDKWGTIDVLNNAGITRDITLLRMKK	171

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QY 175 SQWQDVLDNLTVFLCTQATKVMKKKGKIIINIASVGLTGNVGOANYSAKAGVIG 234
DB 172 SQWDEVIDNLTVFLCTQATKVMKKKGKRIINIASVGLTGNVGOANYSAKAGVIG 231
QY 235 FTKTVAREASRNINNVNAPGFIASDMTAELEKILSTIPLGRYGOPEVAGLVE 294
DB 232 FSKTAAREGASRNINNVNCPGFIASDMTAKLGEDMEKILGTIPLGRYQOPEDVAGLVE 291
QY 295 FLALNPAASVMTQVLTIDGGMW 318
DB 292 FLALSPAASVITQAFITDGGIAI 315

RESULT 2
Q93X62 PRELIMINARY; PRT; 320 AA.
AC Q93X62;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Beta-oxacyl-[acyl-carrier protein] reductase (EC 1.1.1.100).
GN GBRL.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP TISSUE=leaf;
RC TISSUE=Embryo;
RA McDonald F.S., White A.J., Elborough K.M., Slabas A.R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AJ243091; CAC41370.1; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 320 AA; 33671 MW; 3D79CEA41AFFBC49 CRC64;

Query Match 70.18; Score 1093; DB 10; Length 320;
Best Local Similarity 80.78; Pred. No. 2.3e-56;
Matches 213; Conservative 28; Mismatches 23; Indels 0; Gaps 0;

QY 55 VQTHVAVEQAVVVDATKLEAPVTVGASRGIGKATALGKAGCKVLNVARSKEAE 114
DB 57 VKAQATAVEQSTGEAVKVPESPVVVTVGASRGIGKATALGKAGCKVLNVARSKEAE 116
QY 115 EVSKEIASGGEAITFGDVSKEADVESMMKALDKWGTIDVLVNNAGITRDTLLMRKK 174
DB 117 EVSKEIASGGEAITFGDVSKEADVESMMKALDKWGTIDVLVNNAGITRDTLLMRKK 176
QY 175 SQWQDVLDNLTVFLCTQATKVMKKKGKIIINIASVGLTGNVGOANYSAKAGVIG 234
DB 177 SQWDEVIDNLTVFLCTQATKVMKKKGKRIINIASVGLTGNVGOANYSAKAGVIG 236
QY 235 FTKTVAREASRNINNVNAPGFIASDMTAELEKILSTIPLGRYGOPEVAGLVE 294
DB 237 FSKTAAREGASRNINNVNCPGFIASDMTAKLGEDMEKILGTIPLGRYQOPEDVAGLVE 296
QY 295 FLALNPAASVMTQVLTIDGGMW 318
DB 297 FLALSPAASVITQAFITDGGIAI 320

RESULT 3
Q93X67 PRELIMINARY; PRT; 328 AA.
ID Q93X67
AC Q93X67;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)

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DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE 3-oxacyl-[acyl carrier protein] reductase (EC 1.1.1.100).
GN BKR2.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA McDonald F.S., White A.J., Elborough K.M., Slabas A.R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AJ243084; CAC41363.1; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 328 AA; 34373 MW; AFB61AFLIC665545F CRC64;

Query Match 69.18; Score 1078.5; DB 10; Length 328;
Best Local Similarity 73.48; Pred. No. 1.7e-55;
Matches 215; Conservative 31; Mismatches 32; Indels 15; Gaps 2;

QY 28 SRRGFTVFGGAARFSTLRSRGFGSVQTHVAVEQAVVVDK--ATKLEAPVTVVVGASR 85
DB 49 SRPFATSSSTVQ-----AQQAATAEQSTGEAEVAPKVPESPVVVVGASR 95
QY 86 GIGKATALGKAGCKVLNVARSKEAEVSKIEIASGGEAITFGDVSKEADVESMMK 145
DB 96 GIGKATALGKAGCKVLNVARSKEAEVSKIEIASGGEAITFGDVSKEADVESMMK 155
QY 146 AALDKWGTIDVLVNNAGITRDTLLMRKKSQWQDVLDNLTVFLCTQATKVMKKRG 205
DB 156 TVDANGTIDVLVNNAGITRDTLLMRKKSQWDEVIDNLTVFLCTQATKVMKKRG 215
QY 206 KIINIASVGLTGNVGOANYSAKAGVIGFTKTVAREASRNINNVNAPGFIASDMTAE 265
DB 216 KIINIASVGLTGNVGOANYSAKAGVIGFTKTVAREASRNINNVNCPGFIASDMTAK 275
QY 266 LGELEKILSTIPLGRYGOPEVAGLVEFLALNPAASVMTQVLTIDGGMW 318
DB 276 LGEDMEKILGTIPLGRYQOPEDVAGLVEFLALSPAASVITQAFITDGGIAI 328

RESULT 4
Q93X68 PRELIMINARY; PRT; 317 AA.
ID Q93X68
AC Q93X68;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE 3-oxacyl-[acyl-carrier protein] reductase (EC 1.1.1.100).
DE (Fragment).
GN BKR1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA McDonald F.S., White A.J., Elborough K.M., Slabas A.R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AJ243083; CAC41362.1; -.
DR InterPro; IPR002198; ADH_short.

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RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain FCC 7120." ;
RL DNA Res. 8:203-213 (2001).
RL ENBL; AP003587; BABY3593.1; -.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY..
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Complete proteome.
SQ SEQUENCE 251 AA; 26218 MW; 57D0712F8EA6B698 CRC64;

Query Match 50.9%; Score 794.5; DB 16; Length 251;
Best Local Similarity 65.0%; Pred. No. 4.5e-39;
Matches 160; Conservative 30; Mismatches 53; Indels 3; Gaps 1

QY 73 LEAPVVVVTGASRGIGKATALALGKAGCKVLVNYARSKAEAEVSKSEIETGCGEATFGG 132
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 133 DYKSEADYVESNMKKAALDKWGTIDVLVNNAGITDITLLMRMKKSQWODVIDLMLTGVF 192
Db ||||| :||:: ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 68 DVSQVEQVDNLINGAIDKFKRIDILVNNAGITDITLLMRMKPDWQAVDLNLTGVFLCT 127
Db ||||| :||:: ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 193 QAAETKVMKMKKGIINIASVGLTGNVGQANTSAKAGVIGFTKTVAREYASRNINVA 252
Db ||||| :||:: ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 128 RAVSKLMLKQSRGRIINITSVAGQMGNPGQANTSAKAGVIGFTKTVAREYASRNINVA 187
Db ||||| :||:: ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 253 TAPGTIASDWTARIGELEKKILSTIPLRGYGPQPEVAGLVFFLALNPAASYMTGQVLT 312
Db ||||| :||:: ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 188 VAPGFIATDWTSLKSE---GILQYPLGRYGPQPEIAGVWRFLEADPRAAYITGQVFN 244
Db ||||| :||:: ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 313 DGMVM 318
Db ||||| ||||| ||||| |||||
QY 245 DGMVM 250
Db ||||| ||||| ||||| |||||

RESULT 7

```



```
QY 193 QATKVMKKRKGKIINIASVVLGNVGNQYSAKAGVIGFTKTVAEYASRNINVA 252
Db 122 KAVTQMKQKSGRIINVASIVGSGNPGQYAAKAGVIGLTKTSKELASRNILNVA 181
QY 253 IAPGFIASDWTAELEKEKILSTIPGRYQPEVAGLVEFLALNPAASYMTQVLT 312
Db 182 VAPGFISTDMDTQLSKEQDQSLSLVPLERFGKPEDVARVVRFLATED-ANYITQTHI 240
QY 313 DGGWM 318
Db 241 DGGWM 246

RESULT 10
Q8GE35 PRELIMINARY; PRT; 257 AA.
AC Q8GE35
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
DE (Fragment).
OS Helicobacillus mobilis.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;
OC Helicobacillus.
OX NCBI_TaxID=28064;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=22337798; PubMed=12446909;
RA Raymond J., Zhaxybayeva O., Gogarten J.P., Gerdes S.Y.,
RA Blankenship R.E.;
RT "Whole-genome analysis of photosynthetic prokaryotes.";
RL Science 298:1616-1620(2002).
RN [2]
RP Liolios K.G., Chu L., Ostrovskaya O., Mendiyaeva N., Koukharenko V.,
RA Gerdes S., Kyripides N., Overbeek R.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142784; AAN87388.1; -.
KW Oxidoreductase.
FT NON TER 257
SQ SEQUENCE 257 AA; 27163 MW; C68CF5C5AE77C2F7 CRC64;

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Best local similarity 56.0%; Pred. No. 1.4e-33;
Matches 140; Conservative 43; Mismatches 66; Indels 1; Gaps 1;

QY 69 DATKLEAPVVVTGASRGIGKATALGKAGCKVLNVYARSSKEAEVSKIEASGGAEI 128
Db 8 DKMGVLDLTALVTGASRGIGRAIALQALADGFAVAVNYAGSEAKANEVVEIISAGGKAF 67
QY 129 TFGDVSKEADVESMKAALDKWGTIDVLVNNAGITRDTLLMRMKSQWQDVIDNLITGV 188
Db 68 AIOQDVSRQVDVEMQVLAERFDVLVNNAGITRDLNLRKEEDWDVLDNLKGL 127
QY 189 FLCTQATKVMKKRKGKIINIASVVLGNVGNQYSAKAGVIGFTKTVAEYASRN 248
Db 128 FLCSKAIKEMIKORSRIINITSVVGWGNAGQYAAKAGVIGLTKTIAKELSGRNI 187
QY 249 NVNAIAPGFIASDWTAELEKEKILSTIPGRYQPEVAGLVEFLALNPAASYMTQ 308
Db 188 TVNAVAPGYQTDMTDKLSDEVRESLAKTIPGLRQPEVAKVAVFLA-SESAKYITQ 246
QY 309 VLTIDGGWM 318
Db 247 TIINDGGWM 256

RESULT 11
Q8Y690 PRELIMINARY; PRT; 247 AA.
AC Q8Y690
DT 01-MAR-2002 (TReMBLrel. 20, Created)
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DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE FabG protein.
GN FABG OR LMO1807.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Francheul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero P., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefz J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Maca Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001)
DR EMBL; AL591981; CAC99885.1; -.
DR Listlist; LMO01807; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Complete proteome.
SQ SEQUENCE 247 AA; 26248 MW; 539DB67C6C9F5C48 CRC64;

Query Match 44.0%; Score 686.5; DB 16; Length 247;
Best local similarity 55.3%; Pred. No. 9e-33;
Matches 136; Conservative 42; Mismatches 67; Indels 1; Gaps 1;

QY 73 LEAPVVVTGASRGIGKATALGKAGCKVLNVYARSSKEAEVSKIEASGGAEITFGG 132
Db 3 LQKQVAVVTGSGRGIGRDIAINLAKEGANIFFNYNGSPFAAEETAKLVAEHGVEVEMKA 62
QY 133 DVSKRADVESMKAALDKWGTIDVLVNNAGITRDTLLMRMKSQWQDVIDNLITGVPLCT 192
Db 63 NVIAEDVDAPFQAIERFGRVDILVNNAGITRDLNLRMKEDEWDVILNLTGFLCT 122
QY 193 QATKVMKKRKGKIINIASVVLGNVGNQYSAKAGVIGFTKTVAEYASRNINVA 252
Db 123 KAVSRMTMKORAGKIINMASVUGLIGNAGQANVYVASKAGVIGLTKTARELARGINVA 182
QY 253 IAPGFIASDWTAELEKEKILSTIPGRYQPEVAGLVEFLALNPAASYMTQVLT 312
Db 183 VAPGFITDMDTKLDEKTEAMLAQIPLGAYGTTEIDIANAVFLA-SDASKYITGQTLV 241
QY 313 DGGWM 318
Db 242 DGGWM 247

RESULT 12
Q92AK1 PRELIMINARY; PRT; 247 AA.
AC Q92AK1
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE FabG protein.
GN FABG OR LIN1921.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=CLIP 11262 / Serovar 6a;
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RESULT 13
QBR9W0
ID QBR9W0 PRELIMINARY; PRT; 247 AA.
AC QBR9W0;
DT 01-JUN-2002 (TtEMBLrel. 21, Created)
DT 01-JUN-2002 (TtEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TtEMBLrel. 23, Last annotation update)
DE Dehydrogenases with different specificities (Related to short-chain
DE alcohol dehydrogenases).
DE FABG3 OR TTE1472.
OS Thermoanaerobacter tengcongensis.
OC Bacteri; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
RD EMBL; AB013105; AAM24694.1; -.
DR InterPro; IPR002198; ADH short.

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Query Match	42.3%;	Score	659.5;	DB	16;	Length	246;
Best Local Similarity	52.8%;	Pred. No.	3.4e-31;				
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Gaps	1;						
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Db	2	LKDQVAIVTGGTRGIGRAIALKLADQGANIVINYRNSDKAEALKAJLEEGVKVLTKC	61				
Qy	133	DVSKAEADVESNMKAALDKWGTIDVLVNNAGITRDTLLMRMKKSOWQDVIDLNTGVFLCT	192				
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Qy	193	QAATKVMKRRKGKIIINIASVVGITGVNGQANYSAAKAGVIGFTKTVAREVYASRNINVA	252				
Db	122	KHASAIMLKQRFSGKIINNTSVVGIAGNAGQVNYSSASKAGVIGLTKSLAKELGSRGITVNA	181				
Qy	253	IAPGFASIDMTAELGEELEKILSTIPLGRVQGPREEVAGLVEFLALNPAAASYMNGQVLT	312				
Db	182	VAPGFINDMTASLSEKVKKEASKNIPUKRLGDEPDVANLVGFUA-SDAANYITGQVINV	240				
Qy	313	DGGMYM	318				
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 13:14:24 ; Search time 5004 Seconds
(without alignments)
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Title: US-10-024-806-1

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Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: gb_vi.*
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17: em_hum.*
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41: em_hgco_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	489.2	36.9	1186	6	A48348	A48348 Sequence 1
4	487.2	36.7	1159	6	A48349	A48349 Sequence 2
5	478.2	36.1	1124	8	BN243083	AJ243083 Brassica
6	472.4	35.6	1274	8	BN243084	AJ243084 Brassica
7	465	35.1	1276	8	CLCLKR27	X64566 C.lanceolat
8	463.8	35.0	1065	8	AY081491	AY081491 Arabidops
9	463.8	35.0	1234	8	AF324985	AF324985 Arabidops
10	459	34.6	1357	8	AY059816	AY059816 Arabidops
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13	279.4	21.1	343550	1	AP003587	AP003587 Nostoc sp
14	272.2	20.5	11845	1	AE013105	AE013105 Thermoana
15	263.4	19.9	132419	1	D90907	D90907 Synecocyst
16	262.2	19.8	301200	1	AP005374	AP005374 Thermosyn
17	257.8	19.4	2678	1	BSU59433	U59433 Bacillus su
18	256.2	19.3	208780	1	BSUB0009	Z99112 Bacillus su
19	255.4	19.3	450	8	BNB08D	X64463 B.napus mRN
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23	247.2	18.6	303249	1	AP001515	AP001515 Bacillus
24	246.8	18.6	300150	1	AP004598	AP004598 Oceanobac
25	246.8	18.6	302481	1	AE017010	AE017010 Bacillus
26	239.8	18.1	2069	1	D85817	D85817 Staphylococ
27	239.8	18.1	303750	1	AP003133	AP003133 Staphyloc
28	239.8	18.1	347235	1	AP003351	AP003351 Staphyloc
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31	237.4	17.9	741	6	AR108045	AR108045 Sequence
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35	236	17.8	298050	1	AP003189	AP003189 Sequence
36	232.4	17.5	313450	1	AL596170	AL596170 Listeria
37	232.4	17.5	319630	6	AX413016	AX413016 Sequence
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43	217.2	16.4	11523	1	AF197933	AF197933 Streptoco
44	217.2	16.4	12039	1	AE007354	AE007354 Streptoco
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ALIGNMENTS

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LOCUS	AX654380					
DEFINITION	AX654380					
ACCESSION	AX654380.1	GI:29157194				
VERSION	AX654380.1					
KEYWORDS	Oryza sativa					
SOURCE	Oryza sativa					
ORGANISM	Oryza sativa					
REFERENCE	1	Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.				

BNA243085	1185 bp	mRNA	linear	PLN 12-JUN-2001

isoform 3 (bkr3 gene).
AJ243085

AJ243085.1 GI:14422250
3-oxacycl-[acyl carrier
protein] reductase; bkr3 gene.

Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Gymnosperms; Magnoliopsida; Eudicotyledons; Core eudicots;
Rosales; Brassicales

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

Unpublished
2 (bases 1 to 1185)
McDonald E

Direct Submission
Submitted (10-JUN-1999) McDonald F., Department of Biological Sciences, University of Durham, Science Laboratories, South Road, Durham, England, United Kingdom

Durham, DH1 3LE, UNITED KINGDOM	Location/Qualifiers
	1 12.05

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I. .1103
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70. .1017
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36.9%: Score 489.2: DB 8: Length 1185:

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1 Similarity 69.2%; Pred. No. 1.9e-89;
596; Conservative 0; Mismatches 308; Indels 2; Gaps 2;

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31 GGAGCAGCAGCAGTCTCTTCCCTCCGGCTGCGGTGGAGCAGCAGCGGGCGCGCGCGCTCC 240

885 GCAGCAACAAAGCTCACCTCCTTGAAGC-CGTCAAGAGCTCGTTTCGTGAGATCCG 143

44 TCAGGTCGGTCAATGGACTCCGGCTTCAGTCTTCGATGCTCATTTTCGGATCGCGGAGTC 203

000 CGGCCGTGGGTTCTCTGGTGTGCAACCCATGTTGCTGCTGTTGAAACAAGCAGTTGTAA 359

60 AGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTAGTTACAGGTGCATCTAGAGGGATTGG 419

64 AGCTGTTCCGAAAGTGGAGTCTCCGGTGGTCTGCTGTAAGTGGTCTTCGAGAGGGATTGG 323

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CCCG 479

RESULT 4
A48349
LOCUS 1159 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 2 from Patent WO9602652.
ACCESSION A48349
VERSION A48349.1 GI:2302140
KEYWORDS Brassica napus (rape)
SOURCE Brassica napus (rape)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 1159)
AUTHORS Slabas A.R., White A., Chase D., Elborough K. and Fentem, P.A.
TITLE beta-KETOACYL ACP REDUCTASE GENES FROM BRASSICA NAPUS
JOURNAL Patent: WO 9602652-A 2 01-FEB-1996;
ZENECA LTD (GB)
COMMENT Other publication AU 2933695 960216.
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/mol_type="genomic DNA"
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/clone="PUR16.2"
BASE COUNT 315 a 228 c 312 g 304 t
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Query Match 36.7%; Score 487.2; DB 6; Length 1159;
Best Local Similarity 73.9%; Pred. No. 5e-89;
Matches 618; Conservative 0; Mismatches 218; Indels 0; Gaps 0;
QY 290 CGTGGCGTCCGCGCGTGGTCTCTGGTGTGCAACCCACCACTGCTGCTGTGTAACAG 349
DB 141 CGCGGCGAGTCATTCGCACTCCACTGTTGTGAAGCTCAAGCGACAGCTGTGAGCAAT 200
QY 350 CAGTTGTAAAGAGTGTACAGCTGGAAGCTCCAGTGTGTTGTTACAGGTGCACTGA 409
DB 201 CGACAGGAAGCTGTTCCGAAGTGGAGTCTCCGGTGTGTTGTGACTGGTGTCTGA 260
QY 410 GAGGAGTTGGTAGGCAACTGCTAGCCCTTGAAAAAGCAGGATGCAAGTCTGTGTA 469
DB 261 GAGGAGTTGGTAAGCTATGCTCTTCTTCTGGGCAAGCTGGCTGCAAGTCTTGGTGA 320
QY 470 ACTATCCCGGTCTCGAAGAGGCTGAAGAGTCTCCAAAGAGATGAAGCATCTGGTG 529
DB 321 ACTATGCTAGTTCAGCAAGAGGCTGAGGAAGTCTTAAACAGATTTGAAGCATATGGAG 380
QY 530 GTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGAGCTGATGTAGAGTCTATGATGA 589
DB 381 GCCAGGCTATACCTTTGGGGGTGATGTCTCCAAAGAGGCTGATGTGAGGCAATGATGA 440
QY 590 AAGCAGCTCTAGATAAATGGGAAACATAGATGTGCTGTAATAATATGCAAGGATTAAC 649
DB 441 AAACCGCTATTGATGATGATGGGAAACCATTTGATGTGCTGCTCAACATGCGAGGATCACTC 500
QY 650 GAGACATCTGTGATGAGGATGAAGAAATCTCAGTGGCAAGCTGAATTTGATCTCAATC 709
DB 501 GGGATACCTTGTGATGAGGATGAAGAAATGCGCAATGGGATGATTTGATTTGAATC 560
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LOCUS 1124 bp mRNA linear PLN 12-JUN-2001
DEFINITION Brassica napus partial mRNA for 3-oxyacyl-[acyl-carrier protein] reductase, isoform 1 (bkrl gene).
ACCESSION AJ243083
VERSION AJ243083.1 GI:14422246
KEYWORDS 3-oxyacyl-[acyl-carrier protein] reductase; bkrl gene.
SOURCE Brassica napus
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1
AUTHORS McDonald, P.S., White, A.J., Elborough, K.M. and Slabas, A.R.
JOURNAL Unpublished
TITLE Direct Submission
REFERENCE 2 (bases 1 to 1124)
AUTHORS McDonald, P.
TITLE Submitted (10-JUN-1999) McDonald F., Department of Biological Sciences, University of Durham, Science laboratories, South Road, Durham, DH1 3LE, UNITED KINGDOM
JOURNAL Location/Qualifiers
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 LOCUS CLCLR27
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 ACCESSION X64566
 VERSION X64566.1 GI:18045
 KEYWORDS 3-oxoacyl-[acyl-carrier protein] reductase; beta-ketoacyl-ACP reductase; Clikr27 gene.
 SOURCE Cuphea lanceolata
 ORGANISM Cuphea lanceolata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Lythraceae; Cuphea.
 REFERENCE 1 Klein,B., Pawlowski,K., Horicke-Grandpierre,C., Schell,J. and Topfer,R.
 TITLE Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta-ketoacyl-ACP reductase
 JOURNAL Mol. Gen. Genet. 233 (1-2), 122-128 (1992)
 MEDLINE 92293104
 PUBMED 1376402
 REFERENCE 2 (bases 1 to 1276)
 AUTHORS Toepfer,R.
 TITLE Direct Submission
 JOURNAL Submitted (21-FEB-1992) R. Toepfer, MPI f Zuechtungsforchung, Carl-von-Linne-Weg 10, 5000.Koeln 30, FRG
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RESULT 8

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 DEFINITION Arabidopsis thaliana unknown protein mRNA, complete cds.
 ACCESSION AY081491
 VERSION AY081491.1 GI:20148324
 KEYWORDS FLI CDNA
 SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 1065)
 Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M.,
 Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H.,
 Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A.,
 Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K.,
 Sakano, H., Sakurai, T., Satou, M., Seki, M., Shim, P., Yamada, K.,
 Shinozaki, K., Ecker, J.J., Theologis, A. and Davis, R.W.
 Direct Submission

TITLE Submitted (27-FEB-2002) DNA Sequencing and Technology Center,
 JOURNAL Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA

COMMENT comment 'e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN
 Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Nguyen, M.,
 Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J.,
 Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K.,
 Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shim, P.,
 Yamada, K., Ecker, J.J., Theologis, A. and Davis, R.W.

Nguyen, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed
 equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W.
 (SSP/Stanford) contributed equally to this work as PIs.

FEATURES

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LOCUS Arabidopsis thaliana 1234 bp mRNA linear PLN 23-MAY-2001

DEFINITION Arabidopsis thaliana At1g24360 (At1g24360/F21J9_300) mRNA, complete

cds.

ACCESSION AF324985

VERSION AF324985.2

KEYWORDS FLI_CDNA.

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nitrogen-fixing soil bacterium Rhizobium meliloti
Biochem. J. 283 (Pt 2), 321-326 (1992)
JOURNAL 92246853
MEDLINE 1575676
PUBMED
REFERENCE 2 (bases 1 to 1208)
AUTHORS Mackintosh,R.W.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1992) R.W. Mackintosh, Dept of Biochemistry, Univ
of Dundee, Dundee DD1 4HN, UK
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reductase, isoform 4 (bkr4 gene).
ACCESSION AJ243086
VERSION 3-oxoacyl-[acyl carrier protein] reductase; bkr4 gene.
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REFERENCE 1
AUTHORS McDonald,F.S., White,A.J., Elborough,K.M. and Slabas,A.R.
JOURNAL Unpublished
JOURNAL 2 (bases 1 to 927)
AUTHORS McDonald,F.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) McDonald F., Department of Biological
Sciences, University of Durham, Science laboratories, South Road,
Durham, DH1 3LE, UNITED KINGDOM
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QY 468 AAATCTATCCCGGCTCTCGAAGAGGCTGGAAGAGCTCTCCAAAGAGATTGAAGCATCTGG 527
D 130 GAATTATGCTAGGCTGCAAGAGGCTGGAAGAGCTCTCCAAAGAGATTGAAGCATCTGG 189
QY 528 TGGTGAAGCTATCACCTTCGAGGAGAGTTCCTCAAGAGAGCTGATGAGTCTATGAT 587
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ACCESSION AP003587 BA000019
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SOURCE Nostoc sp. PCC 7120
ORGANISM Nostoc sp. PCC 7120
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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AUTHORS Kaneko, T., Nakamura, Y., Wolk, C.P., Kuritz, T., Sasamoto, S., Watanabe, A., Iiguchi, M., Ishikawa, A., Kawashima, K., Kimura, T., Kishida, Y., Kohara, M., Matsumoto, M., Matsuno, A., Muraki, A., Nakazaki, N., Shimo, S., Sugimoto, M., Takazawa, M., Yamada, M., Yasuda, M. and Tabata, S.
Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120
DNA Res. 8 (5), 205-213 (2001)
MEDLINE 21595285
PUBMED 11759840
REFERENCE 2 (bases 1 to 343550)
AUTHORS Kaneko, T.

TITLE Direct Submission
JOURNAL Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research Institute, the First Laboratory for Plant Gene Research; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail: kaneko@kazusa.or.jp,
URL: http://www.kazusa.or.jp/cyanobase/,
Tel: 81-438-52-3935 (ex. 2338), Fax: 81-438-52-3934)
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S-malonyltransferase (EC 2.3.1.39) fabd [validated] -
Bacillus subtilis gi|2337819|emb|CAA74249.1| (Y13937)
putative FabD protein [Bacillus subtilis]
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Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
REFERENCE
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Kaneke, T., Tanaka, A., Sato, S., Kotani, H., Suzuki, T., Miyajima, N.,
Sugliura, M. and Tabata, S.

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TITLE
Sequence analysis of the genome of the unicellular cyanobacterium
Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome
DNA Res. 2 (4), 153-166 (1995)
96127529
PUBMED
8590279
AUTHORS
Kaneke, T., Sato, S., Kotani, H., Tanaka, A., Asanizu, E., Nakamura, Y.,
Miyajima, N., Hirosewa, M., Sugitara, M., Sasamoto, S., Kimura, T.,
Hosouchi, T., Matsuno, A., Muraki, A., Nakazaki, N., Naruo, K.,
Okumura, S., Shimpo, S., Takeuchi, C., Wada, T., Watanabe, A.,
Yamada, M., Yasuda, M. and Tabata, S.
2
TITLE
Sequence analysis of the genome of the unicellular cyanobacterium
Synecocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions
DNA Res. 3 (3), 109-136 (1996)
97061201
PUBMED
8905231
3 (bases 1 to 132419)
Tabata, S.
Direct Submission
Submitted (28-JUN-1996) Satoshi Tabata, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail: tabata@kazusa.or.jp, URL: http://www.kazusa.or.jp/cyano/,
Tel: 81-438-52-3933 (ex.2330), Fax: 81-438-52-3934)
Potential protein coding regions were assigned on the basis of
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Query Match 19.9%; Score 263.4; DB 1; Length 132419;
 Best Local Similarity 59.7%; Pred. No. 5.5e-43;
 Matches 466; Conservative 0; Mismatches 306; Indels 9; Gaps 1;

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Qy	391	GTTCCTTACAGTGCATCTAGAGGATGGTAAGCACTGCTTAGCCCTTGGAAAGCA 450
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Qy	451	GGATGCAAGGTTCCTGGTAAACTATGCCCGGCTCTCGAAAGAGGCTGAAGAGTCTCCAAA 510
Db	96170	GGCATGAAGTGTAGTAGTAATGCTCAATCCAGTACGGCCGCCGATGCTGTGGTAGCG 96229
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Db	96470	ATGCTCAAGCAAAAAAGTGGCGGTATCATTAACATCACTTCTGTAGCGGGCATATGGGG 96529
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Search completed: November 7, 2003, 14:49:07
 Job time : 5011 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 13:13:59 ; Search time 398 Seconds

(without alignments)
8993.605 Million cell updates/sec

Title: US-10-024-806-1

Perfect score: 1326

Sequence: 1 gcgggagcttccaaagcc.....aaaaaaaaaaaaaaaaaa 1326

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 252756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	490.8	37.0	1185	17	AAQ99304 Rape seed beta-ket
2	488.8	36.9	1155	17	AAQ99305 Rape leaf beta-ket
3	403.4	30.4	1053	21	AAC44588 Arabidopsis thalia
4	345.4	26.0	822	21	AAC46385 Arabidopsis thalia
5	254.4	19.2	747	21	AZ45749 Nucleotide sequenc
6	248.4	18.7	294528	24	ABA03041 Listeria monocytog
7	239.8	18.1	6251	18	AAV74336 Staphylococcus aur
8	238	17.9	741	23	AA55438 Staphylococcus aur

9	237.4	17.9	741	21	AAA74685 Staphylococcus aur
10	237.4	17.9	741	22	AAD06206 S. aureus NADPH-de
11	237.4	17.9	741	23	AA555068 Staphylococcus aur
12	237.4	17.9	741	23	AA555365 Staphylococcus aur
13	236.8	17.9	738	23	AA551824 Staphylococcus aur
14	236.2	17.8	929	25	ABT14915 Pathogen specific
15	232.4	17.5	319630	24	ABQ67194 Listeria innocua c
16	232.4	17.5	3011208	24	ABQ69245 Listeria innocua D
17	217.2	16.4	19702	19	AAV52140 Streptococcus pneu
18	217.2	16.4	2162598	25	AB556454 Streptococcus pneu
19	215	16.2	729	25	ABX08055 S. pneumoniae type
20	215	16.2	750	24	ABN92525 Staphylococcus epi
21	214	16.1	3649	22	AAH54361 S. epidermidis gen
22	212.8	16.0	744	24	ABK79267 Bacillus clausii g
23	212.8	16.0	3580	19	AAV65243 S. pneumoniae gene
24	212.2	16.0	2365589	24	ABA90521 Genomic sequence o
25	211.8	16.0	732	21	AAA74684 Streptococcus pneu
26	211.8	16.0	732	22	AAH90731 CFE 35 coding sequ
27	211.8	16.0	732	23	AA553625 Streptococcus pneu
28	211.8	16.0	756	22	AAH90844 2CFE 35 coding seq
29	210.2	15.9	732	23	AA555846 Streptococcus pneu
30	184.4	13.9	1196	19	AA798542 DNA encoding a S.
31	183	13.8	732	24	ABN67976 Streptococcus poly
32	179	13.5	7916	21	AA50142 Bacillus megaterium
33	176.6	13.3	1209	19	AAV37406 Streptococcus pneu
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35	174.2	13.1	2155561	24	ABN71527 Streptococcus poly
36	173	13.0	6021	20	AAH13395 Enterococcus faeca
37	173	13.0	6021	24	AB599190 Enterococcus faeca
38	171	12.9	537	24	ABK79246 Bacillus clausii g
39	166.6	12.6	738	23	AA553187 Enterococcus faeca
40	166.6	12.6	1199	18	AAK30801 Streptococcus pneu
41	158.8	12.0	468	24	ABK74996 Bacillus lichenifo
42	156.8	11.8	735	21	AAZ45746 Nucleotide sequenc
43	156.8	11.8	735	23	AA552392 E. coli DNA for ce
44	156.8	11.8	735	24	ABX17285 DNA encoding Poly3
45	153.2	11.6	1830121	17	AA742063 Haemophilus influe

ALIGNMENTS

RESULT 1
AAQ99304
ID AAQ99304 standard; cDNA to mRNA; 1185 BP.
XX AC AAQ99304;
XX AC
XX 13-APR-1996 (first entry)
XX Rape seed beta-ketoacyl-ACP-ketoreductase PJRS10.1 cDNA.
XX Rape; seed; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase;
XX plasmid PJRS10.1; cDNA library; embryo; Arabidopsis thaliana;
XX probe; hybridization; plasmid rescue; Escherichia coli;
XX poly-A tail; plasmid; stroma; transit peptide; vector; cassette;
XX antisense; oilseed; transgenic plant; crop improvement; lipid;
XX metabolic engineering; polymer; rapeseed oil; ss.
XX Brassica napus.
XX OS
XX Key Location/Qualifiers
XX 5'UTR 1..69
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XX CDS 70..1017 /tag= b
XX mat_peptide 235..1015 /product= Beta-keto-acyl-ACP-ketoreductase
XX 3'UTR 1018..1185 /tag= d
XX /tag= e

XX WO9602652-A2.
PN
XX
XX PD 01-FEB-1996.
XX PF 17-JUL-1995; 95WO-GB01678.
XX PR 20-JUL-1994; 94GB-0014622.
XX PA (ZENE) ZENECA LTD.
XX Chase D, Elborough K, Fentem PA, Slabas AR, White A;
XX WPI; 1996-105914/11.
XX P-PSDB; AAR89322.
XX New isolated rape beta-ketoreductase DNA - used to develop plants
PT with lower or higher oil contents or with altered oil compsn.
XX
XX Claim 1; Page 15; 29pp; English.
XX The sequence corresponds to a rape seed beta-ketoreductase cDNA clone
CC (plasmid pUR510.1 insert). The clone has been isolated by screening
CC of a phage lambda-ZAP rape seed cDNA library, derived from rape Jet
CC Neuf embryo mRNA, with an Arabidopsis thaliana beta-ketoreductase
CC 2.0-kb cDNA probe, subcloning in plasmid pSK and plasmid rescue in
CC Escherichia coli XL1-Blue. The 3'-untranslated region includes a
CC poly-A tail. A plastid stroma targeting transit peptide sequence is
CC present. The DNA may be inserted in a vector or expression cassette
CC in sense or antisense orientation for expression in an oilseed plant,
CC e.g. for production of transgenic rape plants with low or modified
CC oil content, diversion of metabolism to alternative storage
CC compounds, e.g. starch, protein or engineered polymers, or
CC production of plants with enhanced oil content. The DNA may also
CC be used as a probe to obtain similar genes from other plants. The
CC transit peptide DNA may be used in gene fusions to direct other
CC proteins to seed plastids.
XX
XX Sequence 1185 BP; 318 A; 255 C; 303 G; 309 T; 0 other;
SQ
Query Match 37.0%; Score 490.8; DB 17; Length 1185;
Best Local Similarity 69.3%; Pred No. 2.8e-92;
Matches 697; Conservative 0; Mismatches 307; Indels 2; Gaps 2;
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DB 25 CTCCTCTCTCCCTCTCCACCGCTCTCCACCTCTCTCCGCTCCGATGCAACCGCTC 84
QY 181 GCAGCAGCAGCAGCTCTCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 240
DB 85 GCAGCAACAAAGCTCACCTCTCTGAAAGC-CGTCAGAAAGCTCGGTTTCGTGAGATCG 143
QY 241 CGCGGGGTTCGTACGCTTCGTGAGGCGCGCGCGCTCTCTCTCCCA-CGCTGCGGTC 299
DB 144 TCGAGTCGCTCATGACCTCCGCTTCAGTTCGATGCTTCATTCGATCGCGGCGATC 203
QY 300 CGCGCGGTGGTCTCTCTGCTGCAAAACCCATGTTGCTGTTGAAACAGCAGCTTTAAA 359
DB 204 ATTGCAACCTCCACTGTTGTGAAGCTCAAGCGACAGCTGTTGAGCAATCAACAGAGA 263
QY 360 AGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 419
DB 264 AGCTGTTCCGAAAGTGGAGTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 323
QY 420 TAAGGCACTGCTCTAGCCCTTCGAAAGCAGCATGCAAGGTTCTGTGTAACATATGCCCG 479
DB 324 TAAAGCTATTGCT 383
QY 480 GTCTCTCGAAAGAGGCTGAAGAGGCTCTCCAAAGAGATTGAAGCATCTGTTGGTGAGGCTAT 539
DB 384 GTACGCAAGAGGAGGCTGAGGAGTTTCTAAACAGATTGAAGCATATGAGGCCAGGCTAT 443
QY 540 CACCTTCGGAGGAGATGTTTTCAMAAAGAGCTGATGATGATGATGATGATGATGATGAT 599

DB 444 TACTTTTGGGGTGATGCTCTCCAGAGGCTGATGTGGAGCCATGATGAACCCCTAT 503
QY 600 AGATTAATGGGAACAATAGATGTGCTGTAATAATATGAGGATTAACGAGACAT 659
DB 504 TGATGATGGGAACCAATGATGTGCTGCTCAACATGAGGAATCACTCGGATACCTT 563
QY 660 GTTGATGAGGATGAGAAATCTCAGTGGCAAGACGTAATGATCTCAATCTTACTGCGT 719
DB 564 GTTGATACGAATGAGAGATGCCAATGGGATGAAGTATGTTGAAITCTACTGAGT 623
QY 720 CTTCTCTTTGTACACAGCTGCAACAAAGTAATGATGAAAGAGAGAAAGGAAATAT 779
DB 624 CTTCTCTGTACCCAGGCGACACAAAGATCATGATGAAGAGAGAGAAAGGAAATCAT 683
QY 780 CAACATGCAATCTGTATGTTGCTTACTGCAATGTTGGCCAGCTTAATATATAGCCGAC 839
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QY 960 AGAGCTTGAGAGAAATCTTGTCAACCATTCGTTAGGAGATATGCCAACCCAGAGGA 1019
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QY 1020 AGTTGCAAGGTTGCTGCTGAGTTCTTGGGCTTAAACCCGCGAGCTAGCTATATGACTGGACA 1079
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QY 1080 GGTGCTTCAATGACCGAGGATGGAATGTAAGATTGATTTAGTTAG 1125
DB 984 GGCATTCCACCTTATGAGGAGTATTTGCCATCTAGGCATTTGTTAAG 1029
RESULT 2
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XX
AC AAQ99305;
XX
DT 13-APR-1996 (first entry)
XX
DE Rape leaf beta-ketoreductase pURL6.2 cDNA.
XX
KW Rape; leaf; beta-ketoreductase; beta-ketoreductase; beta-ketoreductase;
KW plasmid pURL6.2; cDNA library; Arabidopsis thaliana;
KW probe; hybridization; plasmid rescue; Escherichia coli;
KW plastid; stroma; transit peptide; vector; cassette; antisense;
KW oilseed; transgenic plant; crop improvement; lipid; rapeseed oil;
KW metabolic engineering; polymer; ss.
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OS Brassica napus.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..12 /tag= a
FT transit_peptide 13..177 /tag= b
FT CDS 13..960 /tag= c
FT /product= Beta-ketoreductase
FT mat_peptide 178..960 /tag= d
FT 3'UTR 961..1155 /tag= e
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PN WO9602652-A2.

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PR				
XX	(ZONE) ZENECA LTD.			
PA	Chase D, Elborough K, Pentem PA, Slabas AR, White A;	830	ATAGCGAGCCAGCGCTGGAGTGTGTTTTCACAAAACAGTTGCCAGGGAGTATGCAA	889
XX				
PI				
XX	WPI; 1996-105914/11.	677	ACGCTGCTGCTAAAGCTGGTCTTATTGGGTTCTCCAAGACTGCCGCCAGAGGGGTGCGA	736
DR	P-PSDB; AAR89323.			
XX	New isolated rape beta-ketoreductase DNA - used to develop plants	890	GCAGAAATATCAATGTGAATGCTATTGCACAGGGTTCATTGTCATCTGATATGATGCCG	949
PT	with lower or higher oil contents or with altered oil compen.			
XX	Claim 2; Page 16; 29pp; English.	737	GCAGAAATATCAATGTGAATGCTATTGCACAGGGTTCATTGTCATCTGATATGATGCCG	796
PS				
XX	The sequence corresponds to a rape leaf beta-ketoreductase cDNA	950	AACCTTGGAGAGAGCTTGAGAGAAATCTTGTCAACCATTCCTGTTAGGGAGATATGCC	1009
CC	clone (plasmid pJRL6.2 insert). The clone has been isolated by			
CC	screening of a cDNA library, derived from rape mRNA, with an	797	AGCTTGGAGAGAGCATGGAAGAAATCTTGGGAACAATCCCATTAGGACGATATGGAC	856
CC	Arabidopsis thaliana beta-ketoreductase 0.96-kb cDNA probe,			
CC	subcloning in plasmid pSK and plasmid rescue in Escherichia coli	1010	AACGAGAGAGAGTTCCAGGGTTCGAGTTCCTGGCCCTTAACCCCGCAGCTAGCTATA	1069
CC	present. The DNA may be inserted in a vector or expression cassette			
CC	in sense or antisense orientation for expression in an oilseed	857	AACCTGGAAGATGTGGCTTGGTGTAGTAATCTTGGCTCTCAGTCTCGAGCTAGTTACA	916
CC	plant, e.g. for production of transgenic rape plants with low or			
CC	modified oil content, diversion of metabolism to alternative storage			
CC	compounds, e.g. starch, protein or engineered polymers, or	1070	TCAGTGGACAGTGCTTCAATTTGACGGAGGATGTAATGTAAGATTTGAGTTAG	1125
CC	production of plants with enhanced oil content. The DNA may also be			
CC	used as a probe to obtain similar genes from other plants. The	917	TCACAGGACAGGCATTCACCATTTGATGGAGGATTGGCCATCTAGGCAATTTGTTAAG	972
CC	transit peptide DNA may be used in gene fusions to direct other			
CC	proteins to leaf plastids.			
XX	Sequence 1155 BP; 310 A; 230 C; 309 G; 306 T; 0 other;			
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Query Match 36.9%; Score 488.8; DB 17; Length 1155;				
Best Local Similarity 74.0%; Pred. No. 7.2e-92;				
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QY	290	CGCTGCGGTCGGCGTGGTCTCTGTTGTCGAAACCCCATGTTGCTGTGTTGTAACAAG	349	
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QY	350	CAGTTGTAAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACAGGTGCATCTA	409	
DB	197	CGACAGGAGAGCTGTTCGGAAGTGGAGTCTCCGGTGGTGTGTTGACTGGTCTTGA	256	
QY	410	GAGGATTTGTAAGGCAACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGTCTTGTTAA	469	
DB	257	GAGGATTTGTAAGGCAACTGCTCTCTTCTTGGGCAAGCTGGCTGCAAGGTCTTGGTGA	316	
QY	470	ACTATGCCGCTCTCGAAGAGGCTGAAGAGTCTCCAAAGAGATTGAAGCATCTGGTG	529	
DB	317	ACTATGCTAGTCTAGCAAGAGGCTGAGGAAGTTTCTAAACAGATTGAACATATGGAG	376	
QY	530	GTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGAGCTGATGTAGTCTATGATGA	589	
DB	377	CCAGGCTATTACTTTTGGGGGTGATGCTCCAAAGAGGCTGATGTGGAAGCCATGATGA	436	
QY	590	AAGCAGCTCTAGATAAAATGGGAAACAATAGATGTCTGTGTAATATCCAGGATATCAC	649	
DB	437	AAACCGCTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	496	
QY	650	GAGACATATTGTTGATGAGGATGAGAAATCTCAGTGGCAGACGCTAATGATCTGAATC	709	
DB	497	GCGATACCTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATC	556	
QY	710	TTACTGGGCTCTCTCTTTGTACACAGGCTGCAACAAAAGTATGATGATGATGATGATGATGAT	769	
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Query Match      30.4%; Score 403.4; DB 21; Length 1053;
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XX AC AAC46385;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49949.
XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
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RESULT 6

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XX ABA03041;

DT 05-FEB-2002 (first entry)

DE Listeria monocytogenes EGD-e genome sequence.

XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease; ds.

XX Listeria monocytogenes.

OS WO200177335-A2.

XX 18-OCT-2001.

PD 11-APR-2001; 2001WO-FR011118.

PF 11-APR-2000; 2000FR-0004629.

XX (INSP) INST PASTEUR.

XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
 PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Maduenio E, De Pablos B, Wehlend J, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;

XX WPI; 2002-010914/01.

XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 PT and prevention of Listeria and related bacterial infections, and
 PT related polypeptides

XX Claim 1; SEQ ID No 1; 192pp; French.

XX The present sequence is the genome sequence of Listeria monocytogenes
 CC EGP-e. This sequence and fragments of this sequence are useful for
 CC selecting probes and primers for detecting genes in L. monocytogenes and
 CC related organisms, and to study genetic polymorphisms and other genomes.
 CC Proteins (ABB47297-ABB50149) expressed from the present sequence are
 CC useful for raising specific antibodies, identification of L.
 CC monocytogenes and related organisms, and for biosynthesis and
 CC biodegradation, especially biosynthesis of vitamin B12. This sequence and
 CC proteins encoded by it are also useful for selecting compounds that
 CC regulate gene expression and cell replication and modulate L.

CC monocytogenes-related diseases. In addition, this sequence and proteins
 CC encoded by it are useful in pharmaceutical and vaccine compositions for
 CC the treatment or prevention of infections by L. monocytogenes and related
 CC organisms.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other;

XX Query Match 18.7%; Score 248.4; DB 24; Length 2944528;
 XX Best Local Similarity 58.1%; Pred. No. 3.7e-41;
 XX Matches 457; Conservative 0; Mismatches 326; Indels 3; Gaps 1;

QY 377 AAGTCCAGTTCCTGTTGATCAGGTGATCTAGAGGATGGTAAGCGCACTGCTCTAG 436

DB	1882114	RAAGRAAGTAGCAGTAGCTAACAGGTGGATCAGCGGANTTGGAGCTGACATTTGCCATTA	1882055
QY	437	CCCTTGGAAAAAGCAGGATGCAAGGTTCTGGTAAACATATGCCCGGTCTCTGAAGAGGCTG	496
DB	1882054	ACTTAGCCAAAGAGGCGGAATAATTTCTTCAATTAACAATGGTAGCCAGAGCTGCGG	1881395
QY	497	AAAGGTCTCCAAAGAGATTGAAGCATCTGGTGGTGAGGCTATCATCTTCGGAGGAGATG	556
DB	1881994	AAAGAACAGCAAAATCTCGTTGCTGAACATGGTGTGGAAGTAGAAGCAATGAAGCAACG	1881935
QY	557	TTTCAAAAGAGCTGATGTAGAGTCTATGATGAAAGCAGCTCTAGATAAATGGGAAACAA	616
DB	1881934	TAGCCATTGCCGAAGTGTAGATGCTTTTCAACAAGCAATGTAACGCTTTGGTCGTG	1881875
QY	617	TGATGTGCTGGTAAATAATGACAGGATTACAGGACACATTTGTTGATGAGATGAAGA	676
DB	1881874	TGATATTCTCGTAATAATGGGGAATTTACAGGGGATAATTTATTAATGCGTATGAAG	1881815
QY	677	AATCTCAGTGGCAAGAGCAATTAATGATCTGAATCTTACTCGGCTCTCTTTGTACACAGG	736
DB	1881814	AGACGAATGGGATGACGTTATTAAATCAACCTAAAGAACTTTCCTTTGTACAAAG	1881755
QY	737	CTGCAACAAAAGTAATGATGAAAGAGAGAAAGGAAAAAATTAACAATGCAATCTGTAG	796
DB	1881754	CAGTAAGTCGTACAAATGATGAAACACGCGCAGGTAAATTTATCAACATGGCATCTGTTG	1881695
QY	797	TTGCTCTTACTGGCAATGTTGGCCAAAGCTAATTTATAGCCAGCAAGGCTGGAGTATTG	856
DB	1881694	TTGGTTTGTATTGGTAATGCAAGGTCAAGCAAAATTCGTAGCAAGTAAGCGGCGTTATCG	1881635
QY	857	GTTCACAAAAACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTG	916
DB	1881634	GTTTAAACAAAAACAATCTCTCGAAGAACTTGGCCCGTGGTATTAAGTAATGCTGTTG	1881575
QY	917	CACCAAGGTTCAATGTCATCTGATATGACATGCCGAATCTGGAGAGAGCTTTGAAGAGAAA	976
DB	1881574	CTCCTGGTTTCAATTACAAACAGATATGACAGACAAATTTAGACGAAAAAACAAGAGCA	1881515
QY	977	TCTGTCAACCATTCGTTAGGAGATATGGCCAAACAGAGGAAGTTGAGGTTGGTCG	1036
DB	1881514	TGTTAGCAAAATTCGCTTGGTGTACGAAACAACCGAAGATAATTGCGAATGCAAGTTC	1881455
QY	1037	AGTTCTTGGCCCTTAACCCCGCAGCTAGCTATATGACTGCACAGGTGCTTTACAAATTGACG	1096
DB	1881454	TTTTCTTAGCAAGTGA---TGCTTCGAAGTAATTAATCTGTCAACACTATCCGTTGATG	1881398
QY	1097	GAGGATGGTAATCTAAGATTTGAGTTAGCTTGTGATGCATCTTACTTTTGTGAGCAATTT	1156
DB	1881397	GCGGAATGGTGAATGTAATAATTTGGTTAATGAATGCAATTTTCTTGGCTCGCATTTACTTA	1881338
QY	1157	AATGTT 1162	
DB	1881337	AATATT 1881332	
RESULT 7			
AAV74336			
ID	AAV74336	standard; DNA; 6251 BP.	
XX			
AC	AAV74336;		
XX			
DT	16-MAR-1999	(first entry)	
XX			
DE			
XX			
XX			
KW	Staphylococcus aureus	contig SEQ ID #25.	
KW	Computer readable medium; vaccine; S.aureus infection; immunodetection;		
KW	cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;		
KW	skin infection; surgical wound infection; scalded skin syndrome;		
XX			
OS	Staphylococcus aureus.		
XX			
PH	Key	Location/Qualifiers	

PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELITR-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 PI WPI; 2001-611495/70.
 DR P-PSDB; AAU36529.
 DR
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PS
 PS Claim 27; Seq ID No 8025; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence encodes an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 741 BP; 263 A; 106 C; 165 G; 207 T; 0 other;
 Query Match 17.9%; Score 238; DB 23; Length 741;
 Best Local Similarity 59.0%; Pred. No. 6.3e-40;
 Matches 428; Conservative 0; Mismatches 295; Indels 3; Gaps 1;
 QY 388 GTTGTGTTACAGGTGATCTAGAGGATCGTAGGCACTGCTTAGCCCTTGGAAA 447
 DB 19 GCTTTAGTAACAGGTGATCTAGAGGATCGTAGGCACTGCTTAGCCCTTGGAAA 78
 QY 448 GCAGGATCAAGGTTCTGTTAACTATGCTCCGGGTCCTCGAAGAGGCTGAAGAGTCTCC 507
 DB 79 GAAGGATATATGTAGCAGTAATACATCTAGCAGGACAGAAAGAGCTGAAGCAGTAGTC 138
 QY 508 AAAGAGATTGAAGCATCTGGTGGTGGAGGCTATCACCTCGGAGGAGATGTTCAAAAGAA 567
 DB 139 GAAGAAATCAAGCTAAAGGTTGACAGTTTTGCGATTCAAGCAATGTTGCCGATGCT 198
 QY 568 GCTGATGTAGTCTTATGATGAAGCAGCTCTAGATAATGGGAACAATAGATGCTGTG 627
 DB 199 GATGAAGTTAAAGCAATGATTAAGAGTAGTAGCCATTTGGTCTTTAGATGTTTA 258
 QY 628 GTAAATAATGACGGGATTAACAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGG 687
 DB 259 GTAAATAATGACGGTATTAACGCGATATTTATTATGCGTATGAAGAAACAGAGTGG 318
 QY 688 CAAGACGTAATGATCTGAATCTTACTGGCGTCTTCCTTTGTACACAGGCTCCACAAAA 747
 DB 319 GACGATGTTATTGACACAACTTAAAGAGGTGATTAACTGTATCCAAAAGCAACACCA 378
 QY 748 GTAAATGATCAAAAGAGAGGAGGAAAAATATCAATGTCATCTGTTAGTGGTCTTACT 807
 DB 379 CAAATGTTAAGCAACAGTAGTGGTGCTATCATCAATTTATCAAGTGTGTTGGACAGTA 438
 QY 808 GCAATGTTGGCAAGCTAATATATAGCGCAAGGCTGGAGTGTGTTGTTTCAAAA 867
 DB 439 GGTAAATCCAGGACAAAGCAAACTATGTTGCAACAAAGCAGGTTGTTATTGTTTAACTAAA 498
 QY 868 ACAGTTGCCAGGAGTATGCRAGCAGAAATATCAATGTGAATGCTATTGCACACAGGTTTC 927
 DB 499 TCTGGCGCGCGAATTTAGCATCTCGTGTGATCATCTGTAAATGCAGTTGCACCTGTTT 558
 QY 928 ATTGCATCTGATATGACTCCGAACTTTGAGAGAGAGCTTTGAGAGAAAAATCTTGTCACAC 987
 DB 559 ATTGTTTCTGATATGACAGATGCTTTAACTGATGAGCTTAAGAGACAAATGTTGACTCAA 618
 QY 988 ATTCCGTTAGGAGATATGCGCAACAGAGGAGTTGCGGGTTGTCAGTTCCTGGCC 1047
 DB 619 ATTCCGTTAGCAGCTTTTGGTCAAGACACAGATATTGCTTAATACAGTAGCGTTCTTAGCA 678
 QY 1048 CTTAAACCCGCGAGTAGCTATATGACTGACAGGCTTTTACAATTCACGAGGAGGATGTA 1107
 DB 679 TCAGA---CAAGCAAAATATATTACGTTCAACAAATCAATGTAATGTTGGAATGTAC 735
 QY 1108 ATGTAA 1113
 DB 736 ATGTAA 741
 RESULT 9
 AAA74685
 ID AAA74685 standard; DNA; 741 BP.
 AC AAA74685;
 XX 07-DEC-2000 (first entry)
 DT
 DE Staphylococcus aureus fabG polynucleotide.
 XX
 XX Staphylococcus aureus; fabG; 3-ketoacyl-ACP reductase; antibacterial;
 KW cytosolic; antitumor; cancer; gastric ulcer; gastritis;
 KW Helicobacter pylori infection; microbial infection; ds.
 XX
 OS Staphylococcus aureus.
 Key Location/Qualifiers
 CDS 1..741
 FT /*tag= a
 FT /product= "fabG polypeptide"
 XX
 XX WO200044773-A1.
 XX
 PD 03-AUG-2000.
 XX
 XX 19-JAN-2000; 2000WO-US01196.
 XX
 XX 28-JAN-1999; 99US-0238481.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Huang J, Mcdevitt D;
 XX WPI; 2000-482968/42.
 DR P-PSDB; AAB15707.
 XX
 XX FabG polypeptide, isolated from Staphylococcus aureus, is used to treat
 PT microbial diseases, identify agonists and antagonists for treating
 PT microbial infections and to detect diseases associated with microbial
 PT infections -
 XX
 XX Claim 2; Page 2-3; 37pp; English.
 PS
 XX The present sequence encodes a fabG (3-ketoacyl-ACP reductase)
 CC polypeptide from Staphylococcus aureus. A full length fabG gene was
 CC isolated from an S. aureus WCUH 29 DNA library. fabG polynucleotides
 CC and polypeptides are used for detection and treatment of microbial

CC diseases. They may also be used to identify antagonists and agonists
CC which can then be used to treat microbial diseases. Compounds that
CC interfere with the initial physical interaction between a pathogen and
CC a host have been identified. The compounds are able to prevent the
CC adhesion of bacteria to mammalian extracellular proteins in wounds,
CC prevent adhesion between mammalian extracellular proteins and
CC bacterial fabG proteins which mediate tissue damage and/or to block
CC normal progression of pathogenesis in infections mediated by
CC implantation of in-dwelling devices or other surgical techniques. The
CC fabG polypeptides, polynucleotides, antagonists and agonists are
CC especially useful in the treatment of *Helicobacter pylori* infection.
CC They may be used to decrease *H. pylori*-induced cancers and to prevent,
CC inhibit and/or cure gastric ulcers and gastritis.

XX Sequence 741 BP; 261 A; 105 C; 167 G; 208 T; 0 other;
SQ Query Match 17.9%; Score 237.4; DB 21; Length 741;
Best Local Similarity 58.9%; Pred. No. 8.4e-40;
Matches 428; Conservative 0; Mismatches 236; Indels 3; Gaps 1;

QY 387 TGTGTTGTACAGGTCATCTAGAGGATGGTAAAGCACTGCTTAGCCCTTGAAA 446
DB 18 TGTCTAGTAAACAGTGCATCAAGAGGAATTTGGACGTAGTATTGCGTTACAATTAGCAGA 77
QY 447 AGCAGGATGCAAGTTCTGTGTAACATATGCCGTCTCGAAGAGGCTGAAGGTCCTC 506
DB 78 AGAAGGATATAATGACGATAAATATGACGGCGCAAGAGAACTGAAGCAGTAGT 137
QY 507 CAAAGAGATTGAACATCTGTTGTTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGA 566
DB 138 CGAAGAAATCAAGCTAAAGTGTGACAGTTTTCGATTCAGCAAAATGTCGGATGC 197
QY 567 AGCTGATGTAGTCTATGATGAAGCAGCTCTAGATAAATGCGGAAACAATAGATGTCT 626
DB 198 TGATGAAGTTAAAGCAATGATTAAAGAAAGTAGTAGCCAAATTTGGTTCTTTAGATGCTT 257
QY 627 GGTAAATAATGCGGGATTACACAGACACATTTGATGAGGATGAAGAAATCTCAGTG 686
DB 258 AGTAAATAATGCGAGTATTCTCCGGATAATTTAATGCTGTAAGAAAGAAAGAGAGTG 317
QY 687 GCAGAGCTAATGATCTGATCTTACTGCGGCTCTTCTTTGTACACAGGCTGCAACAAA 746
DB 318 GGATGATGTTATGACACAACTTAAAGGTGTATTAACTGTATCCAAAAGCAACACC 377
QY 747 AGTAATGATGAAGAAAGAGGAAATATACATTCATCTGTAGTTGTCTTTAC 806
DB 378 ACAAATGTTAAGCAACAGTAGTGTGCTATCATCAATTTATCAAGTGTGTTGGCAGT 437
QY 807 TGCAATGTTGGCCCAAGCTAATTATAGCGCAGCAAGGCTGAGTGTGTTTCACAA 866
DB 438 AGGTAATCCGGGACAGCAAACTATGTTGCAAAAGCAGGTGTATTGTTTAACTAA 497
QY 867 AACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGACAGGTT 926
DB 498 ATCTGCGCGGTGAATTAGCATCTCGTGGTATCACTGTAATGCAAGTTCACCTGGTT 557
QY 927 CATTCATCTGATGATGATGCTGCGAACTTGGAGAGAGCTTGAGAGAAATCTGTCAAC 986
DB 558 TATTTGTTTCTGATATGACAGATGCTTTTAAGTGATGAGCTTAAAGACAAATGTTGACTCA 617
QY 987 CATTCGTTAGGAGATATGCCCACAGAGGAGTTGACGGTGTGGTGGAGTTCTTGGC 1046
DB 618 AATTCGTTAGCAGTGTGTTGTTGACAGACAGATATTTCTAATACAGTAGGTTCTTAGC 677
QY 1047 CCTTAACCCCGCAGTATGATGATGCTGAGCAGGTGCTTCAATTTGACGAGGAGTGGT 1106
DB 678 ATCAGA---CAAAGCAAAATATTTACAGGTCAACAACTCCATGTAATGTTGGTAATGTA 734
QY 1107 AATGTAA 1113
DB 735 CATGTAA 741

RESULT 10
AAD06206
ID AAD06206 standard; DNA; 741 BP.
XX
AC AAD06206;
XX
DT 31-JUL-2001 (first entry)
XX
DE S. aureus NADPH-dependent beta-ketoacyl-ACP reductase (FabG) DNA.
XX
KW FabG; high throughput method; fatty acid biosynthesis; therapy;
KW bacterial enzyme; biological agent screening; otitis media; empyema;
KW bacterial tracheitis; acute epiglottitis; thyroditis; lung abscess;
KW infective endocarditis; secretory diarrhoea; splenic; retroperitoneal;
KW intrarenal; perinephric; cerebral; cutaneous; abscess; blepharitis;
KW conjunctivitis; keratitis; endophthalmitis; preseptal; orbital;
KW cellulitis; dacryocystitis; epididymitis; abscess; toxic shock syndrome;
KW impetigo; folliculitis; wound infection; bacterial myositis;
KW septic arthritis; osteomyelitis; beta-ketoacyl-ACP reductase;
KW acyl carrier protein; ds.
XX
OS Staphylococcus aureus 'WCUH 29'.
XX
FH Key Location/Qualifiers
CDS 1..738
FT /tag= a
FT /product= "Staphylococcus aureus FabG"
XX
XX MO200130988-A1.
XX PN
XX PD 03-MAY-2001.
XX
XX 26-OCT-2000; 2000NO-US29451.
XX PF
XX 27-OCT-1999; 99US-0161775.
XX PR
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Dewolf W, Kallender H, Lonsdale JT;
XX
XX WPI; 2001-316332/33.
XX P-PSDB; AAE02195.
XX
XX High throughput method for screening for biological agents against
XX fatty acid biosynthesis comprises contacting a bacterial enzymatic
XX pathway with enzymes e.g. malonyl-CoA:ACP transacylase -
XX
XX Example 16; Page 10; 94pp; English.
XX
XX The present invention relates to a high throughput method for screening
XX biological agents affecting fatty acid biosynthesis, comprises
XX contacting a bacterial enzymatic pathway with enzymes. The method is
XX used for screening biological agents affecting fatty acid biosynthesis.
XX Agonists and antagonists of fab (fatty acid biosynthesis) are used to
XX inhibit, prevent or treat diseases such as infections of the upper
XX respiratory tract (e.g. otitis media, bacterial tracheitis, acute
XX epiglottitis, thyroiditis), lower respiratory (e.g. empyema, lung
XX abscess), cardiac (e.g. infective endocarditis), gastrointestinal (e.g.
XX secretory diarrhoea, splenic abscess, retroperitoneal abscess), central
XX nervous system (e.g. cerebral abscess), eye (e.g. blepharitis,
XX conjunctivitis, keratitis, endophthalmitis, preseptal and orbital
XX cellulitis, dacryocystitis), kidney and urinary tract (e.g.
XX epididymitis, intrarenal and perinephric abscess, toxic shock syndrome),
XX skin (e.g. impetigo, folliculitis, cutaneous abscess, cellulitis, wound
XX infection, bacterial myositis) and bone and joint (e.g. septic
XX arthritis, osteomyelitis).
XX The present sequence is a DNA encoding *Staphylococcus aureus* 'WCUH 29'
XX beta-ketoacyl-ACP (acyl carrier protein) reductase (FabG). In fatty
XX acid biosynthetic pathway, ketoester reduction is by FabG.
XX
XX Sequence 741 BP; 260 A; 105 C; 168 G; 208 T; 0 other;

```
Query Match      17.9%; Score 237.4; DB 22; Length 741;
Best Local Similarity 58.9%; Pred. No. 8.4e-40;
Matches 428; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 387 TGTGTTGTTTACAGGTGCTATCAGAGGATTTGGTAAGGCAACTGCTCTAGCCCTTGGA 446
Db 18 TGTCTTAGTAACAGGTGCTATCAAGAGGAAATGGACGTAGTATTGCGTTACAAATAGCAGA 77
QY 447 AGCAGGATGCAAGGTTCTGTGTAACATATGCCGGTCTCGAAGAGGCTGAGAGGTTCTC 506
Db 78 AGAAGGATATAATGTAGCTAGCAATCTATGCGGAGCAAGAGAGAGAGCTGAAGCAGTAGT 137
QY 507 CAAAGAGATTGAAGCATCTGCTGTAGGCTATCACCTTCGGAGGAGATGTTTCAAGA 566
Db 138 CGAAGAAATCAAGCTAAAGGTGTTGACAGTTTGGCATTCAGCAAAATGTTCCGATGC 197
QY 567 AGCTGATGTAGATCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGTGCT 626
Db 198 TGATGAAGTTAAAGCAATGATTAAGAAAGTAGTTAGCCAAATTTGTTCTTAGATGCTT 257
QY 627 GGTAAATAATCGAGGATTAACAGAGACACATTTGTGATGAGGATGAAGAAATCTCAGTG 686
Db 258 AGTAAATAATCGAGGATTAACAGAGACACATTTGTGATGAGGATGAAGAAATCTCAGTG 317
QY 687 GCAGAGCTAATTCATCTGATCTTACTGCGGTCTCTCTTTGTACACAGGCTGCAAAA 746
Db 318 GGATGATGTTATTGACCAAACTTAAAGGTGTTTAACTGTATCCAAAAGCAGACACC 377
QY 747 AGTAATGATGAAGAGAGAGGAAATATCAACATTCATCTGATGTTGTTCTTAC 806
Db 378 ACAATGTTAAGACACGTAGTGTGCTATCATCAATTTATCAAGTGTGTTGAGCAGT 437
QY 807 TGGCAATGTTGCGCAAGCTAATTAATGCGGAGGCAAGGCTGAGTGAATGTTGTTCAAAA 866
Db 438 AGTAAATCGGAGCAAGCAAACTATGTTGCCAAGGAGGCTGTTATGTTGTTAACTAA 497
QY 867 AACAGTTGCCAGGAGATGCAAGCAGAAATATCAATGTAATCTATGTAATCTTACACAGGTT 926
Db 498 ATCTGCGGCGGTGAATTAATGATCTGCGGTATCACTGTAATGAGTTGACCTGCTGTT 557
QY 927 CATTCGATCTGATGATGCTGCGCAACTTGGAGAGAGCTTGAAGAGAAATCTTGTCAAC 986
Db 558 TATGTTCTGATATGACAGATGCTTTAAGTATGAGCTTAAAGACAAATGTTGACTCG 617
QY 987 CATTCGTTAGGAGATATGGCCACAGAGAGAGTTCAGGGTGTGTCGAGTCTCTGCGC 1046
Db 618 AATTCGTTAGCAGCTTTTGTGTCAGACACAGATATTGCTAATACAGTAGCGTTCTTAGC 677
QY 1047 CTTAAACCCGCGCTAGCTATATGACCTGAGAGGCTGCTTCAATTTGACGAGGATGTT 1106
Db 678 ATCAGA---CAAAGCAAAATATTATACAGGTCAAACAAATCCATGTAATGTTGGAATGTA 734
QY 1107 AATGTAA 1113
Db 735 CATGTAA 741

RESULT 11
AAS55068
ID AAS55068 standard; DNA; 741 BP.
XX
AC AAS55068;
XX
DT 13-FEB-2002 (first entry)
XX
DE Staphylococcus aureus DNA for cellular proliferation protein #1380.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
XX antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN W0200170955-A2.
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XX
PD
XX
PF 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
XX P-PSDB; A037209.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Claim 27; Seq ID No 8705; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the
XX genes, their use in the discovery of novel antibiotics, the essential
XX genes themselves and the encoded proteins. The prokaryotes used are
XX Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX invention is also useful for the identification of potential new targets
XX for antibiotic development. The antisense nucleic acids can also be used
XX to identify proteins used in proliferation, to express these proteins,
XX and to obtain antibodies capable of binding to the expressed proteins.
XX The proteins can be used to screen compounds in rational drug discovery
XX programmes. The antisense nucleic acid sequence is also useful to screen
XX for homologous nucleic acids which are required for cell proliferation in
XX a wide variety of organisms. The present sequence encodes an
XX essential prokaryotic cellular proliferation protein.
XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 741 BP; 261 A; 104 C; 167 G; 209 T; 0 other;

Query Match      17.9%; Score 237.4; DB 23; Length 741;
Best Local Similarity 58.9%; Pred. No. 8.4e-40;
Matches 428; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 387 TGTGTTGTTTACAGGTGCTATCAGAGGATTTGGTAAGGCAACTGCTCTAGCCCTTGGA 446
Db 18 TGTCTTAGTAACAGGTGCTATCAAGAGGAAATGGACGTAGTATTGCGTTACAAATAGCAGA 77
QY 447 AGCAGGATGCAAGGTTCTGTGTAACATATGCCGGTCTCGAAGAGGCTGAGAGGTTCTC 506
Db 78 AGAAGGATATAATGTAGCTAGCAATCTATGCGGAGCAAGAGAGAGAGCTGAAGCAGTAGT 137
QY 507 CAAAGAGATTGAAGCATCTGCTGTAGGCTATCACCTTCGGAGGAGATGTTTCAAGA 566
Db 138 CGAAGAAATCAAGCTAAAGGTGTTGACAGTTTGGCATTCAGCAAAATGTTCCGATGC 197
QY 567 AGCTGATGTAGATCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGTGCT 626
Db 198 TGATGAAGTTAAAGCAATGATTAAGAAAGTAGTTAGCCAAATTTGTTCTTAGATGCTT 257
QY 627 GGTAAATAATCGAGGATTAACAGAGACACATTTGTGATGAGGATGAAGAAATCTCAGTG 686
Db 258 AGTAAATAATCGAGGATTAACAGAGACACATTTGTGATGAGGATGAAGAAATCTCAGTG 317
QY 687 GCAGAGCTAATTCATCTGATCTTACTGCGGTCTCTCTTTGTACACAGGCTGCAAAA 746
```


Db 318 GGATGATGTTATGACACAACTTAAAGGTGTTATTAATCTGATATCCAAAAGCACACC 377
QY 747 AGTAATGATGAAAAAGAGAGGAAAAATTAATCAATTCATCTGTAGTTGGTCTTAC 806
Db 378 ACAATGTTAAGACACAGTAGTGGTCTATCATCAATTTATCAAGTGTGTTGGAGCAGT 437
QY 807 TGGCAATGTTGCCAAGCTAATATATAGCCACCAAGGCTGGAGTGTGTTTACAAA 866
Db 438 AGGTAATCGGACACAGCAAACTATGTTGCAACAAAGCAGGTGTTATGGTTAACTAA 497
QY 867 AACAGTTCACGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGACACAGGGT 926
Db 498 ATCTGGGGCGGTGAATAGCATCTCTGTGTATCACTGTAATGCAATGCACTGGT 557
QY 927 CATTCATCTGATGACTGCCGAATCTGGAGAAGCTTGAAGAAATCTTGTCAAC 986
Db 558 TATTGTTCTGATATGACAGATGCTTAAAGTGTATGATGAGCTTAAAGAACAAATGTTGACTCA 617
QY 987 CATTCGGTTAGGAGATATGGCAACCAAGAGGAGTTCAGGGTGGTTCAGTCTCTGCG 1046
Db 618 AATTCGGTTAGCACGTTTTGGTCAAGACACAGATATTGCTAATACAGTAGCGTTCTTAGC 677
QY 1047 CCTTAACCCCGCAGCTAGCTATATGACTGACACAGGTGCTTACAAATGACGGAGGATGCT 1106
Db 678 ATCAGA---CAAGCAAAATATATTAACAGTCAACATCCATGTAATGGTGGATGTA 734
QY 1107 AATGTAA 1113
Db 735 CAIGTAA 741

RESULT 12

AA55365
ID AA55365 standard; DNA; 741 BP.
AC AA55365;
XX
DT 13-FEB-2002 (first entry)
XX
DE Staphylococcus aureus DNA for cellular proliferation protein #1677.
XX
DE Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.

XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU37506.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Claim 27; Seq ID No 9002; 511pp; English.

XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 741 BP; 261 A; 104 C; 167 G; 209 T; 0 other;

Query Match 17.9%; Score 237.4; DB 23; Length 741;
Best Local Similarity 58.9%; Pred. No. 8.4e-40;
Matches 428; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 387 TGTTCCTTTACAGTGCATCTAGAGGATGTTGAAGCACTGCTTAGCCCTTGGAAA 446
Db 18 TGTTCCTTTACAGTGCATCAAGAGGAATTTGAGCTAGTATTGGCTTACATTAGCAGA 77
QY 447 AGCAGGATCGAAGTTCGTGTAACCTATGTCCTCGAAGAGGCTGAGAGGCTCTC 506
Db 78 AGAAGGATATATGATGACGATTAATCTGACGGCAGCAAGAGAACTGGAAGCAGTAGT 137
QY 507 CAAAGAGATTGAAGCATCTGTGTTGAGGCTATCACCTTCGAGGAGAGATGTTTCAAAA 566
Db 138 CGAAGAAATCAAGCTAAGGTTGACAGTTTGGATTCAAGCAAAATGTTCCGATGC 197
QY 567 AGCTGATGATGATCTATGATGAAGAGCAGCTCTAGATAAATGGGAAACAATGATGCT 626
Db 198 TGATGAAGTTAAGCAATGATTAAAGAGTAGTGTAGCCAAATTTGGTCTTTAGATGTTT 257
QY 627 GGTAAATATGCGAGGATTAACAGACACATTTGTTGATGAGATGAAGAAATCTCAGTG 586
Db 258 AGTAAATATGCGAGTATTACTCGCGATAAATTTAATGCGTATGAAAGAACAGAGTG 317
QY 687 GCAAGACGTAATGATCTGAATCTTACTGGCGTCTTCTTTGTACACAGGCTGCAACAAA 746
Db 318 GGATGATGTTATGACACAACTTAAAGGTGTTATTAATCTGATCCAAAAGCACACC 377
QY 747 AGTAATGATGAAAAAGAGAGGAAAAATTAATCAATTCATCTGTAGTTGGTCTTAC 806
Db 378 ACAATGTTAAGACACAGTAGTGGTCTATCATCAATTTATCAAGTGTGTTGGAGCAGT 437
QY 807 TGGCAATGTTGCCAAGCTAATATATAGCCACCAAGGCTGGAGTGTGTTTACAAA 866
Db 438 AGGTAATCGGACACAGCAAACTATGTTGCAACAAAGCAGGTGTTATGGTTAACTAA 497
QY 867 AACAGTTCGACGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGACACAGGGT 926
Db 498 ATCTGGGGCGGTGAATAGCATCTCTGTGTATCACTGTAATGCAATGCACTGGT 557
QY 927 CATTCATCTGATGACTGCCGAATCTGGAGAAGCTTGAAGAAATCTTGTCAAC 986
Db 558 TATTGTTCTGATATGACAGATGCTTAAAGTGTATGATGAGCTTAAAGAACAAATGTTGACTCA 617
QY 987 CATTCGGTTAGGAGATATGGCAACCAAGAGGAGTTCAGGGTGGTTCAGTCTCTGCG 1046
Db 618 AATTCGGTTAGCACGTTTTGGTCAAGACACAGATATTGCTAATACAGTAGCGTTCTTAGC 677
QY 1047 CCTTAACCCCGCAGCTAGCTATATGACTGACACAGGTGCTTACAAATGACGGAGGATGCT 1106


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Db 678 ATCAGB---CAAGCAAAATATTATACAGGTCAACAATCCATGTAATGGTGGATGTA 734
QY 1107 AATGTAA 1113
Db 735 CATGTAA 741

RESULT 13
AAS51824
ID AAS51824 standard; DNA; 738 BP.
AC AAS51824;
XX
XX
DT 13-FEB-2002 (first entry)
DE
DE Staphylococcus aureus DNA for cellular proliferation protein #241.
XX
XX Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
XX Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US09180.
XX
XX 21-MAR-2000; 2000US-191078P.
XX
XX 23-MAY-2000; 2000US-206848P.
XX
XX 26-MAY-2000; 2000US-207727P.
XX
XX 23-OCT-2000; 2000US-242578P.
XX
XX 27-NOV-2000; 2000US-253625P.
XX
XX 22-DEC-2000; 2000US-257931P.
XX
XX 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX P-PSDB; AAU33965.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Claim 27; Seq ID No 4406; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the
XX genes, their use in the discovery of novel antibiotics, the essential
XX genes themselves and the encoded proteins. The prokaryotes used are
XX Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX invention is also useful for the identification of potential new targets
XX for antibiotic development. The antisense nucleic acids can also be used
XX to identify proteins used in proliferation, to express these proteins,
XX and to obtain antibodies capable of binding to the expressed proteins.
XX The proteins can be used to screen compounds in rational drug discovery
XX programmes. The antisense nucleic acid sequence is also useful to screen
XX for homologous nucleic acids which are required for cell proliferation in
XX essential prokaryotic cellular proliferation protein.
XX
XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 738 BP; 261 A; 106 C; 165 G; 206 T; 0 other;
XX
XX Query Match 17.9%; Score 236.8; DB 23; Length 738;
XX Best Local Similarity 59.5%; Pred. No. 1.1e-39;

Matches 400; Conservative 0; Mismatches 272; Indels 0; Gaps 0;
QY 388 GTTGTGTTACAGGTGTCATCTAGAGGGATGTGTAAGGCAACTGCTCTAGCCCTTGGAAAA 447
Db 19 GCTTTAGTAAACAGGTGTCATCAAGAGGAATTGGACGTAGTATTGCGTTACAATTAGCAGAA 78
QY 448 GCAGGATGCAGGTTCTGTTAACTATGCCCGTCTCGAAGAGGCTGAAGAGTCTCC 507
Db 79 GAAGGATATAATGTAGCAGTAACTATGCAGCAGCAAGAAAAAGCTGAAGACGTAGTC 138
QY 508 AAAGAGATTGAAGCATCTGGTGGTCAAGCTATCACTTCGGAGGAGATGTTTCAAAAGAA 567
Db 139 GAAGAAATCAAGCTAAAGGTGTTGACAGTTTTCGATTCAAGCAAAATGTTCCCGTCT 198
QY 568 GCTGATGTAGACTTATGATGAAGACGCTCTAGATAAATATGGGAAACAATAGATGTCTG 627
Db 199 GATGAAGTTAAAGCAATGATTAAGAGTAGTTAGCCAAATTTGTTCTTTAGATGTTTA 258
QY 628 GTAAATATGCGAGGATTACAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGG 687
Db 259 GTAAATATGCGAGGATTACTCGCATATTTTAAATGCGGTATGAAGAGCAAGAGTGG 318
QY 688 CAAGACGTAATGATCTGAATCTTACTGCGGTCTTCTTGTACACAGCTGCACAAAA 747
Db 319 GACGATGTTATTGACACAAACTTAAAGGTGTTATTAACTGTATCCAAAAAGCAACCA 378
QY 748 GTAATGATGAAGAAAGAGAAAGGAAAAATTAATCAACATTTGCTGTAGTTGGTCTACT 807
Db 379 CAAATGTTAAGACAACGTAGTGTCTATCATCAATTTATCAAGTGTGTTGGAGCAGTA 438
QY 808 GGCATATGTTGGCAAGCTAATTTATAGCGCAGCAAGGCTGGAGTGAATGTTTCAAAAA 867
Db 439 GGTATTCAGGACAGCAAACTATGTTGCCAACAAAGCAGGTGTTATGTTGTTAACTAA 498
QY 868 ACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATCTTATTCACACAGGTTTC 927
Db 499 TCTGGCGCGTGAAATTAGCATCTCGTGTATCACTGTAATGCACTGCACCTGTTTT 558
QY 928 ATTGCATCTGATATGATCTCCGAACTTGGAGAGAGCTTGAAGAAATCTTGTCAACC 987
Db 559 ATTGTTTCTGATATGACAGATGCTTTAAGTATGAGCTTTAAAGAACAAATGTTGACTCA 618
QY 988 ATTCCGTTAGGAGATATGCGCAACCCAGAGGAGTTGCGAGGTTGTCAGTTCCTGGCC 1047
Db 619 ATTCCGTTAGCAGCTTTGTTGTCAGACAGATATTTGCTAATACAGTAGCGTCTTAGCA 678
QY 1048 CTTAACCCCGCA 1059
Db 679 TCAGACAAAAGCA 690

RESULT 14
ABT14915
ID ABT14915 standard; DNA; 929 BP.
XX
XX ABT14915;
XX
XX 06-MAR-2003 (first entry)
XX
XX Pathogen specific antigen related staphylococcal DNA SEQ ID No 117.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis; gene; ds.
XX
XX Staphylococcus sp.
XX
XX WO200259148-A2.
XX
XX 01-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-EP00546.
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XX PR 26-JAN-2001; 2001AT-0000130.
XX PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichhart T, Hafner M;
PI Tempelmaier B;
XX DR WPI; 2003-075410/07.
XX PT Identifying, isolating and producing hyperimmune serum-reactive
PT antigens from a pathogen, for preparing vaccine or medicament for
PT treating or preventing e.g. staphylococcal infections, comprises
PT providing antibody preparation -
XX PS Example 7; Page 163; 252pp; English.
XX CC The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens
CC are used in a vaccine, comprises providing antibody preparation from a
CC plasma pool of a type of animal, or individual sera with antibodies
CC against the specific pathogen, tumour, allergen, tissue or host prone to
CC auto-immunity. The hyperimmune serum-reactive antigens comprising any of
CC the 62 sequences of 53-2261 amino acids fully defined in the
CC specification, or their hyperimmune fragments are useful for the
CC manufacture of a pharmaceutical preparation, particularly a vaccine
CC against staphylococcal infections or colonisation against *S. aureus* or *S.*
CC epidermidis. The preparation of antibodies is useful for the manufacture
CC of a medicament for treating or preventing staphylococcal infections or
CC colonisation against *S. aureus* or *S. epidermidis*. The antibody
CC preparations may also be used for diagnostic and imaging purposes. Other
CC conditions that can be treated include cancer, autoimmune diseases or
CC infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or
CC protozoan pathogens. This polynucleotide sequence represents
CC staphylococcal DNA relating to the method for identifying and producing
CC pathogen specific antigens of the invention.
XX SQ Sequence 929 BP; 331 A; 128 C; 218 G; 252 T; 0 other;
Query Match 17.8%; Score 236.2; DB 25; Length 929;
Best Local Similarity 59.4%; Pred. No. 1.6e-39;
Matches 400; Conservative 0; Mismatches 273; Indels 0; Gaps 0;
387 TGTGTGTTACAGGTGCATCTAGAGGATTTGGTAAGCAACTGCTCTAGCCCTTGGAAA 446
209 TGCTTAGTAACAGGTGCATCAGAGGAATTTGAGGTAGTATTGGTTACAATTAGCAGA 268
447 AGCAGGATGCAAGTTCTGTTAACTATGCGCGTCTCTGAAAGAGGCTGAAGGTCCTC 506
269 AGAAGGATATAATGTAGCAGTAACTATGCGAGGAGCAAGAGAAAGCTGAAGCAGTAGT 328
507 CAAAGGATTTGACCACTCTGTGTGTAGGCTATCACCTTCGAGGAGATGTTTCAAAGA 566
329 CGAAGAAATCAAGCTAAAGTGTGTGAAGTTTTCGATTCACCAATGTTCCGATGC 388
567 AGCTGATGTAGTCTATGATGAAGCAGCTCTAGATAAATGGGCAACAATAGATGTGCT 626
389 TGATGAGTTAAAGCAATGATTAAGAGTAGTTAGCAATTTGTTCTTTAGATGTTT 448
627 GGTAAATAATCGAGGATTTACAGAGACACATTTGTGATGAGGATGAAGAAATCTCAGTG 686
449 AGTAAATAATCGAGTATTACTCGCATATTTTAAATGCGTATGAAGAAACAAGAGTG 508
687 GCAAGACGATTAATGATCTGATCTTACTGCGGTCTCTCTTTGTACAGGCTGCAACAAA 746
509 GCATGATGTTATTGACACAACTTAAAGGTTGTTTAACTGTATCCAAAAGCAACACC 568
747 AGTAATGATGAAGAAAGAGAAAGGAAATATCAACATTCATCTGTAGTGTGCTTTAC 806
569 ACAAATGTTAGACAAACGAGTAGTGTGCTCATCATCAATTTATCAAGTGTGTTGGAGCAGT 628

QY 807 TGGCAATCTGGCCCAAGCTAATTATAGCGCAGCCAGGCTGGAGTGAATGGTTTCACAAA 866
DB AGTAAATCGGACCAAGCAAACTAATGTTGCAACAAGAGAGGTGTTATGTTTAACTAA 688
QY 867 AACAGTTGCCAGGGAGTATCAAGCAGAAATATCAATGTGAATGTATTTGCAACAGGTT 926
DB ATCTCGGCGGTGAATTAGCATCTCGTGGTATCACTGTAAATGCGATTTGACCTGGTTT 748
QY 927 CATTCATCTGATATGACTCGCAACTTGGAGAGAGCTTGAGAGAAATCTTCTCAAC 986
DB TATTTCTTGTATGACAGATGCTTTAAGTGATGAGCTTAAAGAACAAATTTGACTCA 808
QY 987 CATTCGTTAGGAGATATGCGCAACAGAGAGAGTTCAGGGTTTGGTGGAGTTCTCTGC 1046
DB AATTCGTTAGCACGTTTGGTCAAGACACAGATATGCTAATACAGTAGAGCTTCTTAGC 868
QY 1047 CCTTAACCCCGCA 1059
DB 869 ATCAGACAAAGCA 881
RESULT 15
ABQ67194
ID ABQ67194 standard; DNA; 319630 BP.
AC ABQ67194;
DT 29-AUG-2002 (first entry)
XX Listeria innocua contig DNA sequence #7.
DE Antibiacterial; Listeria; food contamination; mutational analysis;
KW infection; ds.
XX Listeria innocua.
XX WO200228891-A2.
XX 11-APR-2002.
XX 04-OCT-2001; 2001WO-FR03061.
XX 04-OCT-2000; 2000FR-0012697.
XX (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX Kunst F, Glaser P;
XX WPI; 2002-332479/37.
XX New genomic sequences from *Listeria* species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators -
XX Claim 5; SEQ ID 7; 180pp; French.
XX The present invention relates to nucleic acid sequences
CC (ABQ67188-ABQ71212) from *Listeria* sp. The sequences are useful as probes
CC and primers for identification and/or detection of *Listeria* (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of *Listeria* (potential therapeutic agents), also for
CC treating infections by *Listeria*, and are useful as immunogens in
CC anti-*Listeria* vaccines.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 319630 BP; 105207 A; 55428 C; 66726 G; 92263 T; 6 other;
Query Match 17.5%; Score 232.4; DB 24; Length 319630;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 13:17:54 ; Search time 93 Seconds
(without alignments)
6293.269 Million cell updates/sec

Title: US-10-024-806-1
Perfect score: 1326
Sequence: 1 ggcggaggtccaaagccc.....aaaaaaaaaaaaaaaaaa 1326

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	488.8	36.9	1155	3	US-08-793-035-2
3	237.4	17.9	741	3	US-09-238-481-1
4	237.4	17.9	741	4	US-09-572-810A-1
5	217.2	16.4	19702	4	US-08-961-527-7
6	215	16.2	750	4	US-09-134-001C-1988
7	211.8	16.0	732	4	US-09-239-052-1
8	184.4	13.9	1196	4	US-08-858-207A-8
9	179.8	13.6	768	4	US-09-107-532A-1296
10	153.2	11.6	1830121	4	US-09-557-884-1
11	153.2	11.6	1830121	4	US-09-643-990A-1
12	150.4	11.3	5395	4	US-09-221-017B-383
13	139.4	10.5	10303	4	US-09-634-238-410
14	139.4	10.5	1230025	4	US-09-198-452A-1
15	132.8	10.0	867	4	US-09-252-991A-1887
16	132.8	10.0	1089	4	US-09-252-991A-2074
17	132	10.0	789	4	US-09-328-352-835
18	126.2	9.5	474	4	US-09-724-623-23
19	117	8.8	4403765	3	US-09-103-840A-2
20	117	8.8	4411529	3	US-09-103-840A-1
21	112.8	8.5	6977	4	US-08-178-257-8
22	112.2	8.5	804	4	US-08-134-001C-2205
23	110.4	8.3	1723	1	US-08-241-766-1
24	110.4	8.3	1723	1	US-08-241-766-2
25	110.4	8.3	2232	1	US-08-241-766-12
26	110.4	8.3	3120	1	US-08-491-146-1
27	110.4	8.3	3120	1	US-08-241-766-11

Sequence 1, Appli
Sequence 1, Appli
Sequence 1675, Ap
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 9, Appli
Sequence 191, App
Sequence 12, Appl
Sequence 3, Appli
Sequence 10, Appl
Patent No. 5229279
Patent No. 5512669
Sequence 10188, A
Sequence 10, Appl
Sequence 1151, Ap
Sequence 24, Appl
Sequence 2, Appli

28 110.4 8.3 3120 1 US-08-234-011-1
29 110.4 8.3 3120 2 US-08-701-062A-1
30 109 8.2 792 4 US-09-134-001C-1675
31 102.8 7.8 786 4 US-09-468-738A-28
32 102.8 7.8 786 4 US-09-940-019-28
33 102.8 7.8 786 4 US-09-940-037A-28
34 102.6 7.7 3252 4 US-09-672-749-9
35 100.6 7.6 15393 4 US-09-453-702B-191
36 98.2 7.4 2675 4 US-09-636-791A-12
37 94.8 7.1 1721 1 US-08-241-766-3
38 94.8 7.1 3051 1 US-08-241-766-10
39 94 7.1 2044 6 5229279-3
40 94 7.1 2094 6 5512669-3
41 92.6 7.0 1311 4 US-09-252-991A-10188
42 90.8 6.8 2535 4 US-09-672-749-10
43 89.2 6.7 828 4 US-09-107-532A-1151
44 87.6 6.6 741 1 US-08-241-943-24
45 87.6 6.6 990 1 US-08-254-357-2

ALIGNMENTS

RESULT 1
US-08-793-035-1
; Sequence 1, Application US/08793035
; Patent No. 6011201
; GENERAL INFORMATION:
; APPLICANT: Siabas, Antoni R.
; APPLICANT: White, Andrew
; APPLICANT: Chase, Dianne
; APPLICANT: Elborough, Keiran
; APPLICANT: Fenem, Phillip A.
; TITLE OF INVENTION: B-Retocyl ACP Reductase Genes From
; TITLE OF INVENTION: Brassica Napus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,035
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9414622.2
; FILING DATE: 20-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB95/01678
; FILING DATE: 17-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1185 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-793-035-1

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Query Match      36.9%; Score 489.2; DB 3; Length 1185;
Best Local Similarity 69.2%; Pred. No. 6.1e-105;
Matches 696; Conservative 0; Mismatches 308; Indels 2; Gaps 2;

QY 121 CTCCTCTTCGGCTCTTCGGTCCGACGCGCCCTCATGCGCACCGCCGCGCCGCA 180
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Db 25 CTCCTCTCTTCGGTCCGACGCGCCCTCATGCGCACCGCCGCGCCGCA 84
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QY 181 GCAGCAGCAGCAGCTCTCTCCCGGTCGCGTGGAGCAGCGCGGGCGCGCGCTCC 240
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Db 85 GCAGCAGCAGCAGCTCTCTCCCGGTCGCGTGGAGCAGCGCGGGCGCGCGCTCC 143
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QY 241 CGCGGGGGTTCGTCAGCTTGGTGGAGCGCGCGCGCTCTCTCTCCCA-CGCTGGGTC 299
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QY 300 CGCGCGTGGTTCCTGCTGTCGCAACCCCATGCTGCTGCTGTAACAACAGCTGTGAAA 359
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Db 204 ATTGCAACCTCCACTGTTGTAAGCTCAAGCAGCAGCTGTTGAGCAATCGACAGAGA 263
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QY 360 AGATGCTTACCAAGTGAAGCTCCAGTGTGTTGTTTACAGTGCATCTAGAGGATTGG 419
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Db 264 AGCTGTTCCGAAAGTGGAGTCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323
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QY 420 TAAGGCAACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGGTTCTGTAACTATGCCCG 479
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Db 324 TAAAGCTATTGCTCTTCTTGGGCAAGGCTGCTGCAAGGCTTGTGTGAAGTATGCTAG 383
    |||
QY 480 GTCTCTGAAAGAGCTCAAGAGGCTCCAAAGAGATTGAAGCACTGCTGTGAGGCTAT 539
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Db 384 GTAGCAAGAGGCTGAGGAGTCTTCAACAGATTGAAGCACTGAGGCGGCTAT 443
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QY 540 CACTTCGAGGAGATGTTTCAAAAGAGCTGATGTGAGAGTCTGTAAGTGAAGAGCTCT 599
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QY 600 AGATAATGGGACAAATAGATGCTGTAATGCTGTAATGCTGTAATGCTGTAATGCTGTA 659
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QY 780 CAACATTCGATCTGCTAGTGTGCTTACTGCGCAATGTTGGCAAGCTAATATAGCGCAGC 839
    |||
Db 684 CAACATTCGCTAGTGTGCTTACTGCGCAATGTTGGCAAGCTAATATAGCGCTGCTGC 743
    |||
QY 840 CAAGGCTGGAGTGTGTTTCAAAAACAGTGTGCGGAGGAGTATGCAAGCAAGATAT 899
    |||
Db 744 TAAAGCTGCTGTTATGCGGTTCTCAAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGG 803
    |||
QY 900 CAATGTGAATGCTATGCAAGGCTTCAATGCTGATGATGATGCTGCGGAGCTTGGAGA 959
    |||
Db 804 AAATGTCAATGTGTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 863
    |||
QY 960 AGAGCTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1019
    |||
Db 864 AGACATGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 923
    |||
QY 1020 AGTTCAGGCTTGGTTCGAGTTCCTGGCCCTTAAACCCCGCAGCTAGCTATATGCTGACA 1079
    |||
Db 924 TGTGCTTGGCTTGGTGAATCTTGGCTCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 983
    |||
QY 1080 GGTGCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1125
    |||
Db 984 GGCATTCACCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1029
    |||

RESULT 2
US-08-793-035-2
; Sequence 2, Application US/08793035
; Patent No. 6011201
; GENERAL INFORMATION:
; APPLICANT: Slabas, Antoni R.
; APPLICANT: White, Andrew
; APPLICANT: Chase, Dianne
; APPLICANT: Riborough, Keiran
; APPLICANT: Fentem, Phillip A.
; TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
; TITLE OF INVENTION: Brassica Napus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,035
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9414622.2
; FILING DATE: 20-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB95/01678
; FILING DATE: 17-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-793-035-2

Query Match      36.9%; Score 488.8; DB 3; Length 1155;
Best Local Similarity 74.0%; Pred. No. 7.5e-105;
Matches 619; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 290 CGCTCGGCTCCGCGCGTCTCTGCTGTGCAAAACCCATGTTGCTGCTGTTGAAACAAG 349
    |||
Db 137 CGCGGAGCTCATTCGCAACCTCCACTGTTGTGAAGCTCAAGCGACAGCTGTTGAGCAAT 196
    |||
QY 350 CAGTTGTAAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTGTTGTTGTTGTTGTTG 409
    |||
Db 197 CGACAGGAGAGCTGTTCGAAAGTGGAGTCTCCGGTGTGCTGTTGCTGCTGCTGCTGCTG 256
    |||
QY 410 GAGGGATGTGAAGCAACTGCTAGCCCTTGGAAAGCAGAGTCAAGAGTTCTGCTGTA 469
    |||
Db 257 GAGGGATGTGAAGCTATTGCTCTTTCCTTGGGCAAGCTGCTGCAAGCTCTTGTGTA 316
    |||
QY 470 ACTATGCCGCTCTCGAAAGAGCTCAAGAGGCTCTCAAGAGATTGAAGCATCTCGTG 529
    |||
Db 317 ACTATGCTAGCTGAGCAAGAGGCTGAGGAGTTTCTAAACAGATTGAAGCATATGAG 376
    |||
QY 530 GTGAGGCTATCACCTTCGAGGAGAGATGTTTCAAAAGAGCTGATGTAGATCTATGAGA 589
    |||
Db 377 GCCAGGCTATTACTTTTGGGGGTGATGCTCTCCAAAGAGGCTGATGTGCGAAGCCATGATGA 436
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QY 590 AAGCAGCTCTAGATAAATCGGGAACAATAGATGCTGCTGTAATATGATGAGGATACAC 649
Db 437 AAACCGCTATTGATGATCGGGAACAATGATGCTGCTGTAATATGATGAGGATACAC 496
QY 650 GAGACACATTTGTTGATGAGGATGAGGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATC 709
Db 497 GGGATACCTTTGTTGATGAGGATGAGGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATC 556
QY 710 TTACTGGCGTCTTCTTCTTGTGATGAGGATGAGGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATC 769
Db 557 TCATCGAGTCTTCTTCTTGTGATGAGGATGAGGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATC 616
QY 770 GAAAAATATCAATGATGATGAGGATGAGGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATC 829
Db 617 GAAGAATATCAATGATGATGAGGATGAGGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATC 676
QY 830 ATAGCGCAGCAAGGCTGAGGATGAGGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATC 889
Db 677 ACCTGCTGCTAAAGCTGATGAGGATGAGGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATC 736
QY 890 GCGAATATCAATGATGATGAGGATGAGGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATC 949
Db 737 GCGAATATCAATGATGATGAGGATGAGGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATC 796
QY 950 AACTTGGAGAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1009
Db 797 AGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
QY 1010 AACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1069
Db 857 AACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 916
QY 1070 TGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1125
Db 917 TCACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 972
```

RESULT 3

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US-09-238-481-1
; Sequence 1, Application US/09238481
; Patent No. 6110704
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: FabG
; FILE REFERENCE: GM10192
; CURRENT APPLICATION NUMBER: US/09/238,481
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-238-481-1
```

Query Match 17.9%; Score 237.4; DB 3; Length 741;
Best Local Similarity 58.9%; Pred. No. 2.8e-46;
Matches 428; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

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QY 387 TGTGTGTTTACAGGTGATCTAGAGGATTTGTAAGCAACTGCTCTAGCCCTTGGA 446
Db 18 TGCTTTAGTAACAGGTGATCTAGAGGATTTGTAAGCAACTGCTCTAGCCCTTGGA 77
QY 447 AGCAGGATGCAAGGTTCTGTTAACTATGTCGCGGTCTCGAAGAGGCTGAAGAGTCTC 506
Db 78 AGAAGGATATATGATGAGGATTTGTAAGCAACTGCTCTAGCCCTTGGA 137
QY 507 CAAAGAGATTTGAAGCATCTGTTGGTGGAGGCTATCACCTTCGGAGGAGATGTTTCAAAGA 566
Db 138 CGAAGATATCAAGCTTAAAGGTTGACAGTGTTCGAGTTCAGGATTCAGCAATGTTCCGATGC 197
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RESULT 4

```
US-09-572-810A-1
; Sequence 1, Application US/09572810A
; Patent No. 6365387
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: FabG
; FILE REFERENCE: GM10192
; CURRENT APPLICATION NUMBER: US/09/572,810A
; CURRENT FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 09/238,481
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-572-810A-1
```

Query Match 17.9%; Score 237.4; DB 4; Length 741;
Best Local Similarity 58.9%; Pred. No. 2.8e-46;
Matches 428; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

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QY 387 TGTGTGTTTACAGGTGATCTAGAGGATTTGTAAGCAACTGCTCTAGCCCTTGGA 446
Db 18 TGCTTTAGTAACAGGTGATCTAGAGGATTTGTAAGCAACTGCTCTAGCCCTTGGA 77
QY 447 AGCAGGATGCAAGGTTCTGTTAACTATGTCGCGGTCTCGAAGAGGCTGAAGAGTCTC 506
Db 78 AGAAGATATCAAGCTTAAAGGTTGACAGTGTTCGAGTTCAGGATTCAGCAATGTTCCGATGC 137
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US-09-134-001C-1988
; Sequence 1988, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1988
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1988

Query Match 16.2%; Score 215; DB 4; Length 750;
Best Local Similarity 56.9%; Pred. No. 4.7e-41;
Matches 414; Conservative 0; Mismatches 310; Indels 3; Gaps 1;

QY 387 TGTGTGTGTACAGGTGCTAGAGGATTTGTAAGGCACTGCTCTAGCCCTTGAAA 446
DB 27 TGTGTGTGTACAGGTGCTCTCGTGTATTTGTAAGGATTTGCAATTCGGA 86
QY 447 AGCAGATGCAAGGTTCTGTAACTATGCGCGTCTCGAAAGAGCTGAAGAGTCTC 506
DB 87 AGAGATATATGTAGTGTCAATTTATGCTGAAGTAAGATAAGCAGACGCTTGT 146
QY 507 CAAAGAGATTAAGCATCTGGTGGGAGGCTATCACCTTCGAGGAGATGTTTCAAAGA 566
DB 147 TGAAGAAATTTAAAGTAAAGGTGTAGAAAGCTTTGCAATACAAAGCAAGTTTCAAAGG 206
QY 567 AGCTGATGTAGCTTATGATGAAGCAGCTCTAGATAAATGGAAGCAATAGATGCT 626
DB 207 CGATGAAGTTAAAGAAATGATTAAGAAAGTGGTAAGTCAAGTGTCTGATGATTT 266
QY 627 GGTAAATATGAGGATTAACAGAGACATTTGTTGATGAGGATGAAGAAATCTCAGTG 686
DB 267 GGTAAATATGAGGATTAACAGAGACATTTGTTGATGAGGATGAAGAAATCTCAGTG 326
QY 687 GCAAGACGTAAATGATCTGAATCTTACTGCGCTCTTCTTTGATACAGGCTGCAAAA 746
DB 327 GGATGACGTGATTTGATACGAATTTAAAGGCGTGTAACTGTATTTCAAAGAGTAACGCC 386
QY 747 AGTAATGATGAAGAAAGAGGAAATATCAATTTGATGAGGATGAAGAAATCTCAGTG 806
DB 387 ACAATTTGCGTCAACGTATGCTGCAATTTAATTTAAGTATTTGCTGCTTAC 446
QY 807 TGGCAATTTGGCCAACTAATATAGCGAGCAAGCTGGAGTGTGTTTTCAAA 866
DB 447 GGGTAATCTGGCAACCAACTATTTGCAACAAAGCAGGTGTCTATTTGAATTAACAA 506
QY 867 AACATTTGCCAGGAGTATGCAAGCAAAATATCAATGTAATGCTATTTGCAACAGGTT 926
DB 507 AACTGCAGCAGAGAACTAGCATCACAGGATTTACAGTGAACGCTTAGCACCTGTTT 566
QY 927 CATTGATCTGATGATGCTGCGCACTTGGAGAGGCTTGGAGAGAAATCTTGTCAAC 986
DB 567 CATCGTTTGAAGATATGCGCAACAGAGAGTGTGAGGTTTGTGCGAGTTCTCTGGC 626
QY 987 CATTCCGTTGAGGATATGCGCAACAGAGAGTGTGAGGTTTGTGCGAGTTCTCTGGC 1046
DB 627 AATTCCCTTTAAAGCTTTTGGAGAGATACAGATATAGCTATTAATCTGCTTCTAGC 686
QY 1047 CCTTAACCCGAGCTAGCTATATGACTGGACAGGTTGCTTACAAATGACAGGAGGATG 1106
DB 687 TTCTGA---TAAAGCTAAATATATACAGGCCCAACCAATTCATGTTAAAGCGTGAATGA 743

QY 1107 AATGTAA 1113
DB 744 TATGTAA 750

RESULT 7
US-09-239-052-1
; Sequence 1, Application US/09239052
; Patent No. 6346395
; GENERAL INFORMATION:
; APPLICANT: Holmes, David J.
; APPLICANT: Zhong, Yiyi
; APPLICANT: Debouck, Christine
; APPLICANT: Jaworski, Deborah D.
; APPLICANT: Wang, Min
; APPLICANT: Warren, Richard L.
; APPLICANT: Kosmatka, Anna L.
; APPLICANT: McDevitt, Damien
; APPLICANT: Ingraham, Karen A.
; APPLICANT: Chalker, Alison F.
; APPLICANT: So, Chi Young
; APPLICANT: Wallis, Nicola G.
; APPLICANT: Pearson, Stewart C.
; FILE REFERENCE: GM10191
; CURRENT APPLICATION NUMBER: US/09/239,052
; CURRENT FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-239-052-1

Query Match 16.0%; Score 211.8; DB 4; Length 732;
Best Local Similarity 58.2%; Pred. No. 2.6e-40;
Matches 394; Conservative 0; Mismatches 277; Indels 6; Gaps 1;

QY 370 AGCTGGAAGCTCCAGTGTGTTGTTTACAGGTGATCTAGAGGATTTGTAAGCAACT 429
DB 4 AAATAGAACATAAAATATCTTTATACAGGTTGAGTGGGAATGGTCTTGCCTC 63
QY 430 GCTTAGCCCTTGGAAAGCAGATCAAGTTCGTGTAATCTATCCCGCTCTCGAAA 489
DB 64 GCCACAGATTTGCTCAGCAGAGCCACATGTTCTTAAACAGTCTGGGCGC-----A 117
QY 490 GAGGCTGAAGAGGTTCTCCAAAGAGATTGAAGCATCTGGTGGTGAAGCTATCACCTTCGGA 549
DB 118 ATCTCAGAAGAAATTTGCTGCTGAGTTTCAAACATATGTTATCAAGGTGTTCCCAATTCA 177
QY 550 GGAGATGTTTCAAAGAGCTGATGTAGTCTATGATGAAGCAGCTCTAGATAATGG 609
DB 178 GGAGATGTTATCAGATTTTTCAGACGCTAAGCGTATGATTTGATCAAGCTATTCAGAACTG 237
QY 610 GGAACAATAGATGCTGCTGTAATATGAGGATTTACAGGATTTACAGAGACATTTGTTGAGG 659
DB 238 GGTTCAGTGAATGTTTGTTCACATGAGGATTTACCAAGATCTCTTATGCTCAAG 297
QY 670 ATGAAGAAATCTCAGTGGCAAGCGTAATTTGATCTGAAATCTTACTGGGCTTCTTCTTGT 729
DB 298 ATGACAGAAGCAGATTTTGAAGAAAGTGTCAAGGTCAATCTGACTGCTGCTTAAATATG 357
QY 730 ACACAGCTGCAACAAAGTATGATGAAGAGAGAAAGGAAATATTCACATTTGCA 789
DB 358 ACACAATCAGTCTTGAAGACCGATGATGAAGCCAGAGAGGTTCTATCATTAATATGCT 417
QY 790 TCTGTAGTGTCTTACTGCAATTTGGCAGCTAAATTTATAGCGCAGCAAGGCTGGA 849
DB 418 AGTGTGTTGTTGATTTGGGGAATATTTGTCAGAGTAACTATGCTGCTTCTAAGGCTGGC 477
QY 850 GTGATTTGGTTTCAAAAAACAGTTGCGAGGAGTATGCAAGCAGAGAAATATCAATGTGAAT 909

Db 478 TTGATTGGCTTTACCAAGTCTGTGGCAGCGGAGGTGCTAGTGGGAATATACAGTCAAT 537
Qy 910 GCTATTGGACACCGGTTTCATTGTCATCTGATATGACTGCCGAACTTGGAGAAAGAGCTTTGAG 969
Db 538 GTGATTGCTCCAGGATGATTGAGTCTGATATGACAGCTATCTTATCAGATAGATTAG 597
Qy 970 AGAAAACTTTGTCAACCATTCCTCGTTAGGGAGATATGGCCAAACGAGAGGAGTTGACGG 1029
Db 598 GAAGCTACACTAGCTCAGATTCGATGCAAGAAATTTGGGCGAGCAGAGGTTGACAGAT 657
Qy 1030 TTGGTCGAGTCTCTGGC 1046
Db 658 TTGACAGTATTTTAGC 674

RESULT 8

US-08-858-207A-8
; Sequence 8, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017670
; FILING DATE: 14-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1196 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-858-207A-8

Query Match 13.9%; Score 184.4; DB 4; Length 1196;
Best Local Similarity 58.4%; Pred. No. 7.9e-34;
Matches 362; Conservative 0; Mismatches 251; Indels 7; Gaps 2;

Qy 353 TTGTAAGAGTGTACCAAGCTGAGCTCCAGTGTGTGTTTACAGGTCATCTAGAG 412
Db 572 TTGAAGGAAAAAATGAACTAGAACATAAAATATCTTTTACAGGTTGAGTCGTG 631
Qy 413 GGATTGGTAAGCAACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGGTTCTGGTAAACT 472
Db 632 GAATTGGTCTGGCCATCGCCCAACAGTTTGTCTACAGCAGGACCAATCTCTTAACA 691

Qy 473 ATGCCCGTCTCGAAAGAGGCTGAAGAGGTCTCAAAGAGATTGAAGCATCTGGTGGT 532
Db 692 GTGCTGGGGC-----AATCTCAGAAGAAATTGCTCGCTGAGTTTCAAACCTATGTTATCA 745
Qy 533 AGGCTATCACCTTCGGAGGAGATGTTCAAAGAAAGCTGATGTAGAGTCTATGATGAAG 592
Db 746 AGGTGGTCCCAATTTCCAGAGATGATCAGATTTTGCAGACGCTAAGCGTATGATGATC 805
Qy 593 CAGCTCTAGATAAATGGGGAACAATAGATGTGCTGTTAAATAATCAGGGATTACACGAG 652
Db 806 AAGCTATTGCAGAACTGGGTTCCAGTAGATGTTTGTCTCAACAATCAGGGATTACCCAAG 865
Qy 653 ACACATTTGATGAGGATGAAGAAATCTCAGTGCAGACGCTAATTTGATCTGAATCTTA 712
Db 866 ATACTCTTATGCTCAAGATGCAGAAAGCAGATTTTGAAGAAAGTGTCAAGGTCATCTGA 925
Qy 713 CTGGGCTCTTCCTTTGTATACACAGGCTGCACAAAAGTAAATGATGAAAAAGAGAAAGGAA 772
Db 926 CTGGTGCCTTTAATATGACAAATCAGTCTTGAACCGATGATGAAGCCAGAGAGGTG 985
Qy 773 AAATTATCAACATTCGATCTGTAGTTGGTCTTACTGGCAATGTTGCCAAGCTAATTATA 832
Db 986 CTATCATTAATATGCTAGTGTGTTGGTTTCATGGGGAATATTGTCGAAGCTAACTATG 1045
Qy 833 GGCAGCCAGGCTGGAGTGAATGTTTCAAAAACAGTTCGCCAGGAGTATGCAAGCA 892
Db 1046 CTGCTTCTAAGGCTGGCTTGGTTTACCAAGTCTGTGGCAGCGAGGTCGTAGTC 1105
Qy 893 GAAATATCAATGTGAATGCTATTGCACACAGG-GTTCATTGCTATGATGATGATGCGCGAA 951
Db 1106 GGAATATACAGTCAATGTGATTTGCTCCAGGAATCATTGATCTGATATGACAGCTATC 1165
Qy 952 CTGGAGAAAGCTTGAGAA 971
Db 1166 TTATCAGATAAGATAAGGA 1185

RESULT 9

US-09-107-532A-1296
; Sequence 1296, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007

```
TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1296:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...768
; SEQUENCE DESCRIPTION: SEQ ID NO: 1296:
US-09-107-532A-1296

Query Match          13.6%; Score 179.8; DB 4; Length 768;
Best Local Similarity 54.6%; Pred. No. 7.8e-33; Indels 15; Gaps 2;
Matches 411; Conservative 0; Mismatches 327;

QY 362 ATGCTACCAAGCTGGAAGCTCCAGTGTGTTGTTACAGTGCATCTAGAGGGATTGGTA 421
Db 26 ACCTTATGGATGTAAGAGGAAAAATGTTATTCACAGGTAGTACAAAGAGGAATCGCA 85
QY 422 AGGCAATGCTTAGCCCTTGGAAAAAGCAGGAGTGCAGGTTCTGGTAAACTATGCCGGT 481
Db 86 AAGCGATGGCTTAGCTTTTGCAAAAGCTGGAGCAAAATATCAATTTGAATGGTCGGGAG 145
QY 482 CCTCGAAGAGGCTGAAGAGTCTCCAAAGAGATTGAGCATCTGGTGGTGAAGCTATCA 541
Db 146 -----AGATTCAAAAGAAAAGATGAGAAATCGAAGCATTCGGGTGTAATATGCCGTAG 199
QY 542 CCTCGAGGAGATGTTTCAAAAGAACTGATGATAGTCTATGATCAAGACGCTCTAG 601
Db 200 GAGTTCCGGTGACATCTCTGATATGAGAAGGGGACAAATGATCAAGAGCAGAAG 259
QY 602 ATAAATGGGAACAATAGATGTGCTGTAATATGATGAGGATTAACAGGACACATGT 661
Db 260 AAAAGCTTGGATGCATCCATGTTGTAGTAAACAATGCGGAATCACAAATGACAACTG 319
QY 662 TGATGAGATGAGAAATCTCAGTGGCAAGCGTAATTTGATCTGAATCTTACTGGCGTCT 721
Db 320 TGATGCAATGGATGCAAGATTTCAAAAATATGCTGGAATCAATTTGATGGAACCT 379
QY 722 TCCTTTGTACACAGCTGCAACAAAGTAATGATGAAAAAGAGAAAGGAAAAATTTATCA 781
Db 380 TCAATATGACGACGACGATTTGAAAAAATGATGAGCAGGAGAGGGGCCATCATTA 439
QY 782 ACATTGCACTGTAGTTGGTCTTACTGGCAATGTTGGCAAGCTTAATATAGCCAGCCA 841
Db 440 ATCTCTAGTGTATCTGGGTGATGGAATAATTTGCTACGAAATTTATGCACTAGTA 499
QY 842 AGGCTGAGTGTATGTTTCAAAAAACAGTTGCCAGGAGTATGCAAGCAAGAAATATCA 901
Db 500 AAGCTGGCGTAGTAGGATTAACAAATCTGTGGCAAGAGAGCTGCAACTAGAGGCATTA 559
QY 902 ATGTGAATGCTATTGCGACAGGGTTCATGTCATCTGATATGACTGCCGAACTTGGAGAAG 961
Db 560 CATGTAATGCCATTGGCGCAGGATTCATCAACAATGATATGACGGAAGTTTAGCAGACA 619
QY 962 AGCTTGAGAAATAATCTTGTCAACCATTCCTGTTAGGAGATATGGCCAAACGAGGAAG 1021
Db 620 AAGTCAAGGAACAAGCGGAAAAGCAATTCGGATGCAAGCGTTTGGCAAGTAGAAGATA 679
QY 1022 TTGCAGGTTGCTCGAGTTCCTGCGCCCTTACCCCGCAGCTAGTATATGACTGACAGG 1081
Db 680 TTGCACAACACGCGAGTTTCTTAGCACAAAATCC-----ATATATCACCGGACAAG 730
QY 1082 TGCTTACAATTTGACGAGGAGTGGTAATGTAAG 1114
Db 731 TCATCAATGTCGATGGCGGATTTGTCATGCAG 763
```

RESULT 10

US-09-557-884-1/c

; Sequence 1, Application US/09557884

; Patent No. 6506581

; GENERAL INFORMATION:

; APPLICANT: Fleischmann et al.

; TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 1/2 inch diskette

; COMPUTER: Dell Pentium

; OPERATING SYSTEM: MS DOS v6.22

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/557,884

; FILING DATE: 25-Apr-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/476,102

; FILING DATE: JUN-5-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Michelle S. Marks

; REGISTRATION NUMBER: 41,971

; REFERENCE/DOCKET NUMBER: PB186P3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1830121 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

; US-09-557-884-1

Query Match 11.6%; Score 153.2; DB 4; Length 1830121;

Best Local Similarity 52.0%; Pred. No. 3.1e-25;

Matches 397; Conservative 0; Mismatches 354; Indels 12; Gaps 2;

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QY 370 AAGCTGGAAGCTCCAGTGTGTTGTTTACAGGTCATCTAGAGGATTTGTAAGGCAACT 429
Db 171555 AAAATGCAGGTAAAAATGCTTTAGTGACAGGATCTACCGTGTGTATCGGTGCGGATT 171496
QY 430 GCTCTAGCCCTCGAAAAGCAGGATGCAAGTTCTGTAACTATGCCGGTCTCTCGAAA 489
Db 171495 GCAGAAGAACTTAGTTCAAAAGG-----TGCATTTGTATTGGTACAGCAACCTCTGAA 171442
QY 490 GAGGCTGAAGAGGTCTCTCAAAGAGATTTGAAGCATCTGGTGGTGAGGCTATCACCTTCGGA 549
Db 171441 AAGGTCACAGCGGATCTCGGCTTAT-----TTAGGGGATAAAGTAAAGGTTTAGTT 171388
QY 550 GGAGATGTTTCAAAGAGCTGATGTAGACTCTATGATGTAAGAGCAGCTCTAGATAAATGG 609
Db 171387 TTAACCGTAACCGGATAAAGAACTCTATCGAAACCTTACTTGAACAAAATTAATAATGATTTT 171328
QY 610 GGAACATAGATGCTGCTGTAATAATATGAGGATTTACAGACACATTTGTTGATCAGG 669
Db 171327 GGCATATTGATATTCTCGTGAATAACGCGAGGTATTACTCGCATTAATTTATTGATCGGT 171268
QY 670 ATGAAGAAATCTCAGTGGCAAGACGTAATGATCTGAATCTTACTGGCGTCTTCTCTTGT 729
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Db 171267 ATGAAGATGAGGAATGGTTGATATATATGCAAACTAACTTAATCTGGTGTATCATCTT 171208
Qy 730 ACACAGCTCTCAACAAAAGTAATGATGAAAAAGAGAAAGGAAAAATTTATCAACATTGCA 789
Db 171207 TCTAAGCCATGTACCTTCATGATGAAAAACGTTTGGTGTATCATCATATTTGGT 171148
Qy 790 TCTGTAGTTGGTCTTACTGCAATGTTGGCAAGCTAAATATAGCGAGCGCAAGGCTGGA 849
Db 171147 TCACTGGTTGGTCTCAACGGGTAAATCCAGGACAACTAACTAATTTGTCGGCAAAAGCGGT 171088
Qy 850 GTGATTTGGTTCAAAAAAGTTCAGGAGGATGCAAGCAGAAATATCAATGTGAAT 909
Db 171087 GTGGTTGGTTTCTTAAATCTTTAGCGAAAGATAGCTGCACGTGTATTTACTGTAAAT 171028
Qy 910 GCTATTGACAGGAGTTCAATGCTATGATGATGCTGCGAACTTTGGAGAGAGCTTTGAG 969
Db 171027 GTGGTTGCTCTCTGTTTATTTGCAACAGATATGACAGAGTGCTTTACGGATGAACMAAA 170968
Qy 970 AAGAAATCTTGTCAACATTCCTGTTAGGAGATATGGCCACAGAGAGGAGTTGCAAGG 1029
Db 170967 GCGGGATCTTATCTAATGTTCCAGCTGGACGTTTAGCGAAGCNAAGACATAGCTAAA 170908
Qy 1030 TTGTCGAGTTCCTGGCCCTTAACCCGCGAGCTAGCTATATGACTGGACAGGTCCTTACA 1089
Db 170907 GCGGTGCTTCTTCTGATGATGCGAGTTATATACGGGAACACGTTACACGCTG 170848
Qy 1090 ATTGACGAGGAGTGTAAATGAAGTTGAGTTAGCTTTGATG 1132
Db 170847 AATGGTGCCTTACTTAAAGCTAAATTTGACATTTGATG 170805

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RESULT 11

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US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof

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; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville,
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,990A
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB186PIC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5790
; TELEFAX: 310-309-8439

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INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

```

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Query Match 11.6%; Score 153.2; DB 4; Length 1830121;
Best Local Similarity 52.0%; Pred. No. 3.1e-25;
Matches 397; Conservative 0; Mismatches 354; Indels 12; Gaps 2;

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Qy 370 AGCTGGAAGTCCAGCTTGTGTTTACAGTGCATCTAGAGGGAATTTGGTAAGGCAACT 429
Db 171555 AAAATCAAGGTAAATATCTTTAGTGACAGGATCTACCCGTTGATCGGTGCGATT 171496
Qy 430 GCTCTAGCCCTTGAAGAAAGCAGGATGCAAGGTTCTGTTAAACTATATCCCGGTCTCGAAA 489
Db 171495 GCAGAAAGAACTTAGTTCAAAGG-----TGCATTTGTAATTGGTACAGCACTCTGAA 171442
Qy 490 GAGGCTGAAGAGGTCTCCAAAGAGATTGAAGCATCTGGTGGTGAAGCTATCACCTTCGGA 549
Db 171441 AAGGTTGCAAGGCGGATCTCGGCTTAT-----TTAGGGGATAAAGGTAAAGGTTAGTT 171388
Qy 550 GAGATGTTTCAAAAGAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 609
Db 171387 TTAACGTTAACGGATAAGAAATCTATCGAAACCTTACTTGAACAAATTTAAATGATTTT 171328
Qy 610 GGAACAATAGATGCTGCTGTAATAATGCAAGGATTTACAGGAGATTACAGACACACATTTGATGAGG 669
Db 171327 GCGATATTGATATTCTCTGATATACGCAAGTATTACTCGCGATAATTTATTGATGCGT 171268
Qy 670 ATCAAGAAATCTCAGTGGCAAGACGTTAATGATGATGATGATGATGATGATGATGATGATG 729
Db 171267 ATGAAGATGAGGAATGGTTTGTATATTAATGCAAACTAACTTAACCTTCGGTGTATCATCTT 171208
Qy 730 ACACAGCTCTCAACAAAAGTAATGATGAAAAAGAGAAAGGAAAAATTTATCAACATTGCA 789
Db 171207 TCTAAGCCATGTAGCTTCAATGATGAAAAAACGTTTGGTGTATCATCATATTTGGT 171148
Qy 790 TCTGTAGTTGGTCTTACTGGCAATGTTGGCAAGCTAAATATATAGCGAGCGCAAGGCTGGA 849
Db 171147 TCACTGGTTGGTTCACGGGTAAATCCAGGACAACTAATCTATTTGTCGGCAAAAGCGGT 171088
Qy 850 GTGATTTGGTTCAAAAAAGTTCAGGAGGATGCAAGCAGAAATATCAATGTGAAT 909
Db 171087 GTGGTTGGTTTCTTAAATCTTTAGCGAAAGATAGCTGCACGTGTATTTACTGTAAAT 171028
Qy 910 GCTATTGACAGGAGTTCAATGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 969
Db 171027 GTGGTTGCTCTCTGTTTATTTGCAACAGATATGACAGAGTGTCTTACGGATGAACMAAA 170968
Qy 970 AAGAAATCTTGTCAACCAATTCGTTAGGGAGATATGCGCAACCCAGAGGAGTTGCAAGG 1029
Db 170967 GCGGGATCTTATCTAATGTTCCAGCTGGACGTTTAGCGAAGCNAAGACATAGCTAAA 170908
Qy 1030 TTGTCGAGTTCCTGGCCCTTAACCCGCGAGCTAGCTATATGACTGGACAGGTCCTTACA 1089
Db 170907 GCGGTGCTTCTTCTGATGATGCGAGTTATATACGGGAACACGTTACACGCTG 170848
Qy 1090 ATTGACGAGGAGTGTAAATGAAGTTGAGTTAGCTTTGATG 1132
Db 170847 AATGGTGCCTTACTTAAAGCTAAATTTGACATTTGATG 170805

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RESULT 12

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US-09-221-017B-383/c
; Sequence 383, Application US/09221017B
; Patent No. 644799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

```

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; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P11182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P11546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P22911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 383:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5395 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...5395
; US-09-221-017B-383

Query Match 11.3%; Score 150.4; DB 4; Length 5395;
Best Local Similarity 51.2%; Pred. No. 1.3e-25;
Matches 377; Conservative 0; Mismatches 356; Indels 3; Gaps 1;

QY 385 GTTGTCTTGTGTTACAGGTGATCTAGAGGGATTGGTAAGCACTGCTTAGCCCTTGA 444
DB 1558 GTAGCTCTATTACGGGACGGCGGTATCGCGGTGCTATAGTATGA 1499

QY 445 AAGCAGATGCAAGTTCTGGTAACTATGCCCGGTCTCGAAGAGGCTGAAGAGTC 504
DB 1498 ACGGAAGTGGCGGATGTGGCTATTACTGATCTGAATATCGATGAGGGCGTACAGGCTTTC 1439

QY 505 TCCAAAGAGATTGAAGCATCTGGTGTGAGGCTATACCTTCGGAGGAGATGTTTCAAAA 564
DB 1438 GTAGAAGAACTCAAGGGCTCGGAGTAGTGCAGGGCATACGCTTCAATGACGGAT 1379

QY 565 GAAGCTGATGATGATCTATGATGAAAGCAGCTCTAGATAAATGGGAAACAATAGATGTG 624
DB 1378 TTCCATGACGACATACATAGTGTGGACAGATCAAGGCTGACTTCGGTCCGATCGATATT 1319

; 625 CTGGTAAATAATGACAGGATTACAGACACATTTGTTGATGAGGATGAAGAAATCTCAG 684
; 1318 TTGGTGAACATGCGCGTATTACTCGCATGCGCTTATGATGCGTATGCCAGCAACA 1259
; 685 TGGCAAGACGTAATTTGATCTGAATCTTACTGCGCTTCTTTGTACAGGCTGCAACA 744
; 1258 TGGGATGCGGTGATCAACGTTAACTCTGAAGTCAGCGTTCAACATGATCCATGCCGTGACT 1199
; 745 AAGTAATGATGAAAAAGAGAGGAAAAATTATCAACATTTGATCTGTTGTTGTT 804
; 1198 CCCATCATGATGGGACAGCGCACCGGAGTATCATCAATATATGCTTCTGTGTAGTGTGA 1139
; 805 ACTGCAATGTTGGCCAAAGCTAATTTATAGCGCAGCAAGGCTGGAGTGAATTTGTTTCA 864
; 1138 TCAGGCAATGACGAGCAATCCACTACTCAGTTTCTAAGCCGGTATGATCGTTTGGCC 1079
; 865 AAAACAGTTGCGAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTTATGCAACGAGG 924
; 1078 AAGAGTGTGCGCAAGAGCTGGGCTCAGTGGCTGCGTGGTCCCAATCGGATTCACCGGCT 1019
; 925 TTCAITGATCTGATATGACTGCCGAACTTGAGAGAGCTTGAGAGAAATCTTGTCAC 984
; 1018 TTTATCATCACCGATATGACTGCCGTCTTACCGAAGAGTGAAGAACATGCGGCGGCA 959
; 985 ACCATTTCGTTAGGAGATATGCCCAACAGAGGAGTTGCGAGGTTGGTCGAGTTCTCTG 1044
; 958 CAGATACCTTCGCTGCTGGTGGTACGCCCGGAGATGGCTTAACTAGTACTTCTT 899
; 1045 GGCCTTTAACCCGCGAGCTAGCTATATGACTGACAGAGGCTTCAATACGAGGAGGATG 1104
; 898 GGCAGTGACCTC--TCTTCGTACGTGACGCGGACAGGTAGTCCACGTTTGGCGGTATG 842
; 1105 GTAAATGATGATTTGA 1120
; 841 AATATGTAATATATAGGA 826

RESULT 13
US-09-634-238-410/c
; Sequence 410, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 410
; LENGTH: 10303
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
; US-09-634-238-410

Query Match 10.5%; Score 139.4; DB 4; Length 10303;
Best Local Similarity 52.8%; Pred. No. 6.1e-23;
Matches 350; Conservative 0; Mismatches 306; Indels 7; Gaps 2;

QY 395 TTACAGGTGATCTAGAGGATTGGTAAGCACTGCTTAGCCCTTGGAAAGCAGGAT 454
DB 6999 TCACCGTGTGCTCACGAGGTATCGGTGAAGCGATTGCCAGAAATTTGCTCAAGCAGGG 6940
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Qy	519	AGCATCTGGTGTGAGGCTATCACTTCGGAGGAGATGTTTCAAAGNAGAGCTGATGTAGA	578
Db	344918	AGGCTTGGGTGGGGAAGTTTCTTTTGTCTCGTGTGTGATGTGAGTCATATATGTTGGAGTGAA	344859
Qy	579	GTCTATGATCAAGACAGCTCTCTAGATAAATCGGGGAACAATAGATGTGCTGGTAAATAATGC	638
Db	344858	AGATTGGGTGCAGAAATTTTGTAGATAAGCAACAATAATAGATATTTTGGTAAATAATGC	344799
Qy	639	AGGGAATPACACGAGACACATTTGTTGATCAGGATCAAGAAATCTCAGTGGCAAGCGTAAT	698
Db	344798	AGCAATACCAGGGATAATTTGTTGATGCGTATCTCTGAGGACGACTGCGCAATCGTGTAT	344739
Qy	699	TGATCTGAATCTTACTGGGCTCTCCCTTTGTPACACAGCTGCCAACAAAGTAATGATGAA	758
Db	344738	TAGCACCACACTTGACTTCTCTTGTATTATACATGTTCTCAGTGATTCGCCATATGATTA	344679
Qy	759	AAAGAGAAAGGGAATAATCAACATTCGATCTGTAGTTGGTCTTACTGGCAATGTTGG	818
Db	344678	GGCGGTTCAGATCTATTAATAATGTGGCTTCTATTGTTGCTAAGATCGGTAGTCCGGG	344619
Qy	819	CCRAGCTAATTTATAGCGCAGCAAGGCTGGAGTGATTGGTTTCAAAAAACAGTTGCCAG	878
Db	344618	CCGACCAACTATGCTGCTGAAGCTGGGATTATGCTTTTCAAAAACTTTTACGTAA	344559
Qy	879	GGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGCCACAGGGTTCATTGCACTGTA	938
Db	344558	GGRAGTAGCTGCAAGAAATATTCTGTCACTGCCCTTCTCCAGGCTTTATTGAAACAGA	344499
Qy	939	TATGACTGCCGAATCTCGAGAGAGCTTGAGAAGAAATCTTGTCAAACATTCCTTAGG	998
Db	344498	CATGACAAGCGTTGTGAATGCAATTTAAAGCTGAGTGGCTTAAAGTCATCCCTTTAGG	344439
Qy	999	GAGATATGGCCAAACAGAGGAAGTTGACGGGTTGGTCGAGTTTCTTGGCCCTTAAACCCCGC	1058
Db	344438	TAGGGCTGGCACTCCAGAGAGATGTTGCTCGTGTGGCGTTGTTTTTAGCC--TCGCA	344382
Qy	1059	AGCTAGCTATANGACTGCAAGGTGCTTACAATTGACGGAGGATGGTAAATGTAGA	1115
Db	344381	ATCCAGCTATATGACCGCGCAGACACTGGTTGTTGTATCGGGGATGACTTACTAGAA	344325

RESULT 15

US-09-252-991A-1887/c
; Sequence 1887, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1887
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1887

Query Match 10.0%; Score 132.8; DB 4; Length 867;
Best Local Similarity 50.0%; Pred. No. 7.6e-22;
Matches 360; Conservative 0; Mismatches 357; Indels 3; Gaps 1;

Qy	342	TGAACAAGCAGTTGTAAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACAGG	401
Db	808	TGAGAGAGAGAAAGGAGAGATCCATGAGTCTCAAGGTAAGGTGCAATTGGTTAACCGG	749
Qy	402	TGCATCTAGAGGATTGGTAGGCACTGCTAGCCCTTGGAAAAAGCAGATGCAAGGT	461
Db	748	CGCCAGCCGTGGCATCGGCCAGGCGATTGGCTGGAATCGGGCGCCTGGGTGCCGTGT	689
Qy	462	TCGTGTAATATATCCCGGTCTCGAAAGAGGCTGAAAGAGGTCTCCAAAGAGATTGAAGC	521
Db	688	CATCGGCACCGGACCCAG--CGCGTCGGCGCCCGAGAGATCGCCGAAACCTCAAGGC	632
Qy	522	ATCTGGTGGTAGGCTATCACCTTCGGAGAGAGATGTTTCAAAGAAGTGATGAGATC	581
Db	631	CAATGGCGTTCGAGGTCGGGCGCTGCTCGAGCGTTTCCAGCGACGAAATCCGTAGCCGC	572
Qy	582	TATGATGAAGCAGCTCTAGATAATGGGGAACATAGATGTGCTGCTTAATATGCAAG	641
Db	571	GACCTGGAGCACAATCCAGCAGCATCTGGGCCAACCGCTGATCGTGGTCAATAACGCCG	512
Qy	642	GATTACACGACACATGTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAAATTGA	701
Db	511	CATCACCGCGATATCTGCTGGTGGCATGAAAGACGACGAGTGGTTCGATGTGTTCAA	452
Qy	702	TCTGAATCTTACTGGCGTCTTCCTTTTACACAGGCTGCAACAAAGTAATGATGAATAA	761
Db	451	CACCAACCTGAACAGTCTCTACCGTCTGTCTGAAAGCCGTTCTGGCGCGTATGACCAAGC	392
Qy	762	GAGAAAGGAAAAATATACATATGATGCTCTGTAGTTGGTCTTACTGGCAATGTCCTCA	821
Db	391	CCGCTGGGGCGGCATCATCAACATCGGTTCGCTGGTGGGCCCATGGGCAATCCGGGCA	332
Qy	822	AGCTAATTTATAGCGCAGCAAGGCTGGAGTGAATGTTTCAAAAAACAGTTGCCAGGA	881
Db	331	AACCACTATGCCGGCGAAGCGCGCTGGAGGGCTTCAACCGTGGCTGGCCCGGA	272
Qy	882	GTATGCAAGCAGAAATATCAATGTGAATGCTATTGCAACAGGGTTCAATTGATCTGATAT	941
Db	271	AGTGGTTTCGGTGCCTTACCGTGAATGCGGTGGCGCGCGGCTTTCATCGACACCGCAT	212
Qy	942	GACTCCGAACTTGAGAGAGCTTGAGAGAAATCTTGTCAACCATTCGTTAGGAG	1001
Db	211	GACCGCGAGCTCCCGGAAGCCACGCGGAAGCGCTGCTGGGCCAGATTCCGCTGGGTG	152
Qy	1002	ATATGGCCAAACAGAGGAGTTGCAAGGTTGGTTCGAGTTCTTGGCCCTTAACCCCGCAGC	1061

Db 151 CCTGGGGCAGGCGGAAGAGATCGCCAAGTGTGCGCTTCCTCGCTTCGGAACGGCGCAGC 92

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Job time : 107 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 14:49:09 ; Search time 441 Seconds
(without alignments)
9594.580 Million cell updates/sec

Title: US-10-024-806-1
Perfect score: 1326
Sequence: 1 ggcggagcttccaaagcccc.....aaaaaaaaaaaaaaaaaaaaa 1326

Scoring table: IDENTITY_NUC

Gapop 10.0 , Capext 1.0

Searched: 2141354 seqs, 1595478879 residues

Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:
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11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:
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17: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	607.4	45.8	1286	12	Sequence 1, Appli
3	431.2	37.0	1398	12	Sequence 3, Appli
4	449.4	33.9	1248	12	Sequence 5, Appli
5	239.8	18.1	6251	8	Sequence 7, Appli
6	238	17.9	741	9	Sequence 25, Appli
7	237.4	17.9	741	9	Sequence 8025, Ap
8	236.8	17.9	741	9	Sequence 8705, Ap
9	236.8	17.9	741	9	Sequence 9002, Ap
10	232.8	16.0	744	10	Sequence 4406, Ap
11	211.8	16.0	732	9	Sequence 6558, Ap
12	210.2	15.9	732	9	Sequence 9262, Ap
13	179	13.5	7916	10	Sequence 9483, Ap
14	175.2	13.2	741	10	Sequence 1, Appli
15	173	13.0	6021	10	Sequence 8, Appli
16	171	12.9	537	10	Sequence 458, App
					Sequence 6537, Ap

17 166.6 12.6 738 9 US-09-815-242-6824
18 158.8 12.0 468 10 US-09-974-300-2287
19 156.8 11.8 735 9 US-09-815-242-6029
20 153.2 11.6 1830121 14 US-10-329-960-1
21 148.4 11.2 744 9 US-09-815-242-7417
22 147.4 11.1 729 9 US-09-815-242-6877
23 146.8 11.1 744 9 US-09-815-242-7245
24 142.8 10.8 804 10 US-09-895-913A-361
25 132.4 10.0 640681 10 US-09-790-988-1
26 130.6 9.8 744 9 US-09-815-242-7795
27 126.2 9.5 474 12 US-10-288-930-23
28 125.2 9.4 786 12 US-10-004-115A-27
29 125.2 9.4 786 12 US-10-327-108-11
30 119.4 9.0 1000 10 US-09-971-536-32
31 115.2 8.7 813 10 US-09-974-300-2254
32 112.2 8.5 1980 12 US-10-166-225A-177
33 109.6 8.3 958 10 US-09-880-107-1741
34 106.8 8.1 29729 10 US-09-070-927A-238
35 106.4 8.0 789 9 US-09-815-242-6500
36 104.4 7.9 714 9 US-09-823-901-3
37 104.4 7.9 714 14 US-10-175-696-15
38 104.4 7.9 1043 9 US-09-823-901-1
39 104.4 7.9 1043 14 US-10-175-696-13
40 102.8 7.8 786 10 US-09-940-037A-28
41 101.2 7.6 1089 14 US-10-119-926-96
42 101 7.6 717 14 US-10-156-761-6439
43 101 7.6 9025608 14 US-10-156-761-1
44 100.6 7.6 729 12 US-10-238-075-836
45 100.6 7.6 15393 14 US-10-114-170-191

ALIGNMENTS

RESULT 1

US-10-024-806-1
; Sequence 1, Application US/10024806
; Publication No. US20030167532A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping
; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; TITLE OF INVENTION: Their Use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/258,417
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)...(1110)
US-10-024-806-1

Query Match 100.0%; Score 1326; DB 12; Length 1326;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGCGAGCTTCCAAAGCCCCCGTCCCAATAGACTCTCCCATCCCGTCTGTCTCC 60
Db 1 GCGCGAGCTTCCAAAGCCCCCGTCCCAATAGACTCTCCCATCCCGTCTGTCTCC 60
QY 61 GTCAAGGCTCAATATCTCGGCTGCACTCTCAAGACACTGTCTGTGGTTCGCG 120
Db 61 GTCAAGGCTCAATATCTCGGCTGCACTCTCAAGACACTGTCTGTGGTTCGCG 120
QY 121 CTCTCTTGGCTCTTGGCTGCTCCGACGCCCTCTATGCGCCACCGCGCCGCGCA 180

Db 121 CTCTCTTCGGCTCCCTCGGCTCCCGACGCCCTCATAGCCACCGCGCGCCACCGCA 180
QY 181 GCAGCAGCAGCTCTCTCCCGGCTCGCGTGGAGCAGCCGCGGCGCGCGCTCC 240
Db 181 GCAGCAGCAGCTCTCTCCCGGCTCGCGTGGAGCAGCCGCGGCGCGCTCC 240
QY 241 CGCGGGGGTTCGTACAGTTGGTGGAGGCGCGCGGCTCTCTCCAGCTCGCGTCC 300
Db 241 CGCGGGGGTTCGTACAGTTGGTGGAGGCGCGCGGCTCTCTCCAGCTCGCGTCC 300
QY 301 GSCCGTGGTCTCTGCTGTGCAACCCATGTTGCTGCTGTGAACAAGCAGTTGAAA 360
Db 301 GSCCGTGGTCTCTGCTGTGCAACCCATGTTGCTGCTGTGAACAAGCAGTTGAAA 360
QY 361 GATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTACAGTGCATCTAGAGGATTTGT 420
Db 361 GATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTACAGTGCATCTAGAGGATTTGT 420
QY 421 AAGCCTACTCTCTAGCCCTTGAAAGCAGGATGCAAGTTCTGTTAACTATGCCCG 480
Db 421 AAGCCTACTCTCTAGCCCTTGAAAGCAGGATGCAAGTTCTGTTAACTATGCCCG 480
QY 481 TCCTCGAAGAGGCTGAAGAGTCTCCAAAGAGATTGAAGCATCTGGTGTGAGGCTATC 540
Db 481 TCCTCGAAGAGGCTGAAGAGTCTCCAAAGAGATTGAAGCATCTGGTGTGAGGCTATC 540
QY 541 ACCTTCGAGGAGATGTTTCAAAAGAGCTGATGAGAGTCTATGATGAAGCAGCTCTA 600
Db 541 ACCTTCGAGGAGATGTTTCAAAAGAGCTGATGAGAGTCTATGATGAAGCAGCTCTA 600
QY 601 GATTAATGGGAAACAATAGATGCTCTGTTAAATATCGAGGATTAACAGACACATTG 660
Db 601 GATTAATGGGAAACAATAGATGCTCTGTTAAATATCGAGGATTAACAGACACATTG 660
QY 661 TTGATGAGGATGAAGAAATCTCAGTGGCAAGCCTAATGATCTGAATCTTACTGGCGTC 720
Db 661 TTGATGAGGATGAAGAAATCTCAGTGGCAAGCCTAATGATCTGAATCTTACTGGCGTC 720
QY 721 TTCCTTTGTACACAGGCTGCAACAAAAGTAATGATGAAGAAAGAGAAAGGAAATATC 780
Db 721 TTCCTTTGTACACAGGCTGCAACAAAAGTAATGATGAAGAAAGAGAAAGGAAATATC 780
QY 781 AAGCTGAGTGTGATGTTTCAACAAAACAGTTCGCGAGGATGCAAGCAGAAATATC 900
Db 781 AAGCTGAGTGTGATGTTTCAACAAAACAGTTCGCGAGGATGCAAGCAGAAATATC 900
QY 901 AATGTGAATGATGATGCAAGGTTGATGCAATGATGATGATGATGATGATGATGATG 960
Db 901 AATGTGAATGATGATGCAAGGTTGATGCAATGATGATGATGATGATGATGATGATG 960
QY 961 GAGCTGAGAGAAATCTCTGCAACCAATCCGTTAGGAGATGAGCAACAGAGAA 1020
Db 961 GAGCTGAGAGAAATCTCTGCAACCAATCCGTTAGGAGATGAGCAACAGAGAA 1020
QY 1021 GTTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 GTTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 GTGCTTCAATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
Db 1081 GTGCTTCAATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 CTTTGTGAGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
Db 1141 CTTTGTGAGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 ATTAGTGTGCTCTCTCTGTTAAATCTCTGTTAAATCTAGCATGTGGAATGGA 1260

Db 1201 ATTAGTGTGCTCTCTCTGTTAAATCTCTGTTAAATCTAGCATGTGGAATGGA 1260
QY 1261 AGTTGAATCTGGTTTCGTGTAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
Db 1261 AGTTGAATCTGGTTTCGTGTAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
QY 1321 AAAAAA 1326
Db 1321 AAAAAA 1326

RESULT 2
US-10-024-806-3
; Sequence 3, Application US/10024806
; Publication No. US20030167532A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping
; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; TITLE OF INVENTION: Their Use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)...(1050)
US-10-024-806-3

Query Match 45.8%; Score 607.4; DB 12; Length 1286;
Best Local Similarity 75.4%; Pred. No. 2.3e-140;
Matches 755; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

QY 118 CGCTCTCTCTCGGCTCTCTCGGCTCCCGACGCGCCCTCATGCGCCACCGCGCCGCCACC 177
Db 58 CTCCT 117
QY 178 GCAGCAGCAGCAGCT 237
Db 118 GCCTCTGCGCACGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 177
QY 238 TCCTGCGCGGGGTTCGTTCAGTTTGGTGGAGGCGCGCGCGCTCTCTCTCTCTCTCTCT 297
Db 178 GCCTGCGCGGGGTTCGTTCAGTTTGGTGGAGGCGCGCGCGCTCTCTCTCTCTCTCTCT 237
QY 298 TCCTGCGCGGGGTTCGTTCAGTTTGGTGGAGGCGCGCGCGCTCTCTCTCTCTCTCTCT 357
Db 238 CGCGCGCT 297
QY 358 AAGATGCTACCAAGCTGAGAGCTCCAGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 417
Db 298 AAGATGCTACCAAGCTGAGAGCTCCAGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 357
QY 418 GGTAAAGCACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGGTTCTGGTAAACTATGCT 477
Db 358 GGTAAAGCACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGGTTCTGGTAAACTATGCT 417
QY 478 CGGTCTCTCGAAGAGGCTGAGAGGCTCTCCAAAGAGATTGAAGCATCTGGTGGTGGCT 537
Db 418 CGATCTTCAAGGAGGCTGAGAGGCTCTCCAAAGAGATTGAAGCATCTGGGAGGCGCC 477
QY 538 ATCACTCTCGAGAGAGATGTTTCAAAAGAGCTGATGATGATGATGATGATGATGATG 597
Db 478 ATTACCTTTGGAGAGATGTTTCCAAAGAGGCTGATGTTGAAATCTATGATAAAGTGGCT 537

NAME/KEY: CDS
LOCATION: (16)... (912)
US-10-024-806-7

Query Match 33.9%; Score 449.4; DB 12; Length 1248;

Best Local Similarity 73.9%; Pred. No. 3.9e-101;
Matches 570; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

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QY 344 AACAGCAGTGTGTAAGAGTGTCTACCAAGCTGGAAGCTCCAGTGTGTTGTTACAGGTG 403
DB 146 AGCTAGACTTGAAGCAGCAGAGACATGAGACACCTGTTGTTAGTCACTGGAG 205
QY 404 CATCTAGAGGATGTGTAAGCAACTGCTCTAGCCCTTGGAAGAGGAGTGCAGGTTTC 463
DB 206 CCTCCAGAGGCAATGGCCGTGCAATGCACTTCTCTGGGTAAAGCCCATGCAAGGTG 265
QY 464 TGGTAAACTATGCCGCTCTCCGAAAGAGGCTGAGAGGTCTCCAAAGAGATGCAAGCAT 523
DB 266 TGGTCAACTATGCCAGGTCACTCCATGCAAGCTGAGGAGGTTCACACTTGATGAGCGT 325
QY 524 CTGCTGTGAGGCTATCACCTTCGAGGAGAGTGTTCAAAGAGAGCTGATGAGTCTA 583
DB 326 TTGTTGGACAGCTTACCTTCGAGGAGAGTGTTCATGAGGCGGATGGAATCTA 385
QY 584 TGATGAAGCAGCTCTAGATAAATGGGAAACATAGATGTCTGCTGGTAAATATGACGGA 643
DB 386 TGATTAGAACTGCAAGTGTGATGCTTGGGGAAGTGTGATGATGTTAAACAAATGAGAA 445
QY 644 TTACACGAGACACATTTGATGAGGATGAAGAATCTCAGTGGCAAGAGCTAATGATC 703
DB 446 TTACTCGAGATGTTGTTAATGAGATGAAGAATCAATGGCAGGAGTATGATC 505
QY 704 TGAATCTTACTGGCGTCTTCTTTGTACACAGGCTGCAACAAAAGTATGATGAAAAGA 763
DB 506 TGAATCTCAGTGTGTTTCTTTGATGAGGAGGAGCAAGAGATTATGACGATGAAA 565
QY 764 GAAAGGAAAATATCAACATGCACTGTAGTTGTTTTCACAAAACAGTCCAGGAGT 823
DB 566 AGAAGGGAAGGATAATCAATATTAATCAGTATTTGGTTCAGGTTGGCAATGTTGACAG 625
QY 824 CTAATTATAGCGCAGCAGGCTGAGTGTGTTTTCACAAAACAGTCCAGGAGT 883
DB 626 CCAATTATGCTCTCAAGGAGGAGTGTGCTCAAAAAGTCTGCCAGGAT 685
QY 884 ATGCAAGCAGAAATATCAATGCTATGCTATGCAACAGGTTCAATGCACTGATGA 943
DB 686 ATGCTAGCAGAAACATCACTGTTAATGCACTAGCCCTGGTATTGCACTGATGA 745
QY 944 CTGCCGAATCTGGAGAAGCTTGAGAGAAATCTTGTCAACCATTCGTTAGGAGAT 1003
DB 746 CTGCCAATCTAGCACCGCATTTGAGAAAAGATGGAATTAATCCCTTAGGAAGAC 805
QY 1004 ATGGCCCAACAGGAAGTTGAGGTTGCTGAGTTCCTGCGCTTAAACCCCGCAGCTA 1063
DB 806 TTGGCCCAACAGGAAGTTGCTGAGTGTGGAATTTCTGGCTTTAATCTCTGCTGCA 865
QY 1064 GCTATATGACTGGACAGGTGCTTACAATGACGAGGAGTGAATGAAG 1114
DB 866 ATTACATCACTGGCAGGTGTTCAACATTTGATGAGGAGTTGGCAATGTGAG 916
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RESULT 5

US-08-781-986A-25
Sequence 25, Application US/08781986A
Publication No. US20030054436A1

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville

STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 6251 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-781-986A-25

Query Match 18.1%; Score 239.8; DB 8; Length 6251;

Best Local Similarity 56.7%; Pred. No. 1.1e-48;

Matches 442; Conservative 0; Mismatches 337; Indels 0; Gaps 0;

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QY 387 TGTGTGTTTACAGGTGTCATCTAGAGGATGTGTAAAGCAACTGCTCTAGCCCTTGAAA 446
DB 4316 TGTGTGTTTACAGGTGTCATCTAGAGGATGTGTAAAGCAACTGCTCTAGCCCTTGAAA 4375
QY 447 AGCAGGATGCAAGGTTCTGGTAAACTATGTCGCGGTCTCGAAAGAGGCTGAAGAGTCTC 506
DB 4376 AGAAGGATATAATGTTAGCAGTAAACTATGTCAGGCGAGCAAGAGAAAGCTGAAGCAGTAGT 4435
QY 507 CAAAGAGATTGACGATCTGTTGAGGCTATCACTTCGGAGGAGATGTTTCAAGA 566
DB 4436 CGAAGAAATCAAAGCTAAAGGTGTTGACGTTTTCGAGTTTCAGCAAAATGTCGCGATGC 4495
QY 567 AGCTGATGAGTCTATGATGAAAGCAGCTCTAGATAAATGGGAAACAAATAGATGTGCT 626
DB 4496 TGATGAGTTTAAAGCAATGATTAAGAGAGTAGTTAGCCAAATTTGGTCTTTTAGATGTTT 4555
QY 627 GGTAAATAATGCGAGGATTCACGAGACACATTTGTTGATGAGGATGAAGAATCTCAGTG 686
DB 4556 AGTAAATAATGCGAGTATTACTCGGATAATTTAATGCGTATGAAGAACCAAGAGTG 4615
QY 587 GCAGAGTAAATGATCTGATCTTACTGGGCTCTTCTTTGTACACAGGCTGCAACAA 746
DB 4616 GGATGATGTTTATTGACACAACTTTAAAGGTGTTAATTAATCTGATCAAAAGCAACACC 4675
QY 747 AGTAAATGATGAAAAGAGAAAGGAAAAATATCAACATTTGCACTCTGTAGTTGTCTTAC 806
DB 4676 ACAAATGTTAAGCAACAGTAGTGTGCTATCATCAATTTATCAAGTGTGTTGGAGCAGT 4735
QY 807 TGGCAATGTTGGCAAGCTAATTAAGCGCAGCAGCAGGCTGGAGTGTGTTTCAAAA 866
DB 4736 AGGTAATCCGCGACAGCAAACTATGTTGCAACAAAGCAGGTGTTTGGTTTAACTAA 4795
QY 867 AACAGTTGCCAGGAGTATGCAACAGAAATATCAATGTGATGCTATTGACACAGGTT 926
DB 4796 ATCTGCGCGGTGAATTAGCATCTCGTGGTATCACTGTAAATGCACTGACCTGGTTT 4855
QY 927 CATGTCATCTGATATGACTGCCGAACCTTGGAGAGAGAGCTTCAGAGAAAGAAATCTTGTCAAC 986
DB 4856 TATTGTTCTGATATGACAGATGCTTAAAGTATGAGCTTAAAGAACAAATGTTGACTCA 4915
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QY 987 CATTCGGTAGGAGATATGGCCACACAGAGAGGAGTTGCGAGGTTGGTCGAGTTCTCTGC 1046
DB 4916 AATTCGGTTAGCACGTTTTGGTCAAGACACAGATATTTGCTAATACAGTAGCGTTCTTAGC 4975
QY 1047 CCTTAACCCGCGAGCTAGCTATATGACTGACACAGGTCCTTACAAATGACGAGGATGCT 1106
DB 4976 ATCAGAACAAAGCAAAATATATACAGGTCMAACAATCCAGTAAATGGTGGATGTACAT 5035
QY 1107 AATGTAAAGATTGAGTTAGCTTGATGCATCTTACTTTTCTGAGCATTTAATGTTGAA 1165
DB 5036 GTAAATATTTGAGCTAAAGCTCATTCGACGCGATGTTGACTGGTCATCCATGAGAA 5094

RESULT 6

US-09-815-242-8025
; Sequence 8025, Application US/09815242
; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8025

; LENGTH: 741

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(741)

; US-09-815-242-8025

Query Match 17.9%; Score 238; DB 9; Length 741;
Best Local Similarity 59.0%; Pred. No. 8.9e-49;
Matches 428; Conservative 0; Mismatches 295; Indels 3; Gaps 1;

QY 388 GTTCTGTTACAGTGCTAGAGGATTTGGTAAGCACTGCTTAGCCCTTGGAAAA 447
DB 19 GCTTTAGTAACAGGTGCTCAAGAGGATTTGGCTAGTATTTGGTTACATTAACAGAA 78
QY 448 GCAGATGCAAGTTCTGGTAACTATGCGCGCTCCGAAAGAGGCTGAAGAGTCTCC 507
DB 79 GAAGATATATGATGACGATTAATCTGACGCGAGCAAGAAAGCTGAAGCAGTAGTC 138
QY 508 AAAGAGATTAAGCATCTGGTGGTGGAGCTATCACCTTCGGAGGAGATGTTTCAAAAGAA 567
DB 139 GAAGAAATCAAGCTAAAGGTGTTGACAGTTTGGATTCAGCAATGTTGCCGATGCT 198

QY 568 GCTGATGTAGAGTCTATGATGAAGACAGCTCTAGATAAATGGGGAACAATAGATGTGCTG 627
DB 199 GATGAAGTTAAGCAATGATTAAGAGTAGTTAGCCAAATTTGGTTCTTTAGATGTTTA 258
QY 628 GTAAATAATGCAAGGATTACACAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGG 687
DB 259 GTAAATAATGCAAGGATTACTCGCATTAATTTATTAATGCGTATGAAAGAACACAGAGTGG 318
QY 688 CAAAGAGTAATTTGATCTGAATCTTACTGGCGCTTCTCTTCTTTGACACAGCTCCACAAA 747
DB 319 GACGATGTTATTGACACAAACTTAAAGGTGTTTAACTGTATCCAAAAGCAACACCA 378
QY 748 GTAAATGATGAAGAGAAAGGAAAAATTATCAACATTCGCTCTGTAGTTGGTCTTACT 807
DB 379 CAATGTTAAGCAACAGTAGTGTGCTATCATCAATTTATCAAGTTGTTGGAGCAGTA 438
QY 808 GCAATGTTGGCCAGCTTAATTTATGCGCAGCAAGGCTGGAGTGATGTTGTTTCAAAA 867
DB 439 CGTAATCCAGGACAAAGCAACTATTTGCAACAAAGCAGGTTGTTATTGTTTAACTAAA 498
QY 868 ACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGCAACCGAGTTC 927
DB 499 TCTGCGGCGCGTGAATTAGCATCTCGTGTATCATCTGTAATGCAAGTTCACCTGGTTT 558
QY 928 ATTGCATCTGATATGACTGCCGAACTTGAGAGAGAGCTTGAGAAAGAAATCTTGTCAACC 987
DB 559 ATGTTTCTGATATGACAGATGCTTTAAGTGTAGCTTTAAGACAAATGTTGACTCAA 618
QY 988 ATTCCGTTAGGAGATATGCCCAACACAGAGAGTTGCGAGGTTGGTCAGTTCTGGCC 1047
DB 619 ATTCCGTTAGCAGGTTTGGTCAAGACACAGATATTTGCTAATACAGTAGCGTTCTTAGCA 678
QY 1048 CTTAACCCCGAGCTAGCTATATGACTGACAGGTCCTTACATTTACAGGAGGATGTA 1107
DB 679 TCAGA---CAAGCAAAATATATTACAGGTCAAAACAATCCATGTAATGTTGAATGTAC 735
QY 1108 ATGTAA 1113
DB 736 ATGTAA 741

RESULT 7

US-09-815-242-8705
; Sequence 8705, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16

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; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8705
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(741)
US-09-815-242-8705

Query Match      17.9%; Score 237.4; DB 9; Length 741;
Best Local Similarity 58.9%; Pred. No. 1.3e-48;
Matches 428; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 387 TGTGTGTTGTACAGGTCATCTAGAGGATTTGGTAAGGCAACTGCTCTAGCCCTTGAAA 446
Db 18 TGCTTTAGTAACAGGTGCATCAAGAGAAATGGACGTAGTATTGGTTACAATTAGCAG 77
QY 447 AGCAGATGCAAGGTTCTGTGTAATGATGCGGTCCTCGAAAGAGGCTGAAGAGTCTC 506
Db 78 AGAAGGATATAATGTAGCAGTAACTATGCGGCGCAAAAGAGAAAGCTGAAGCAGTAGT 137
QY 507 CAAAGAGATTGAAGCATCTGGTGCAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGA 566
Db 138 CGAAGAAATCAAAGCTTAAAGGTTGTGACAGTTTGGCATTTCAAGCAAAATGTCGGATGC 197
QY 567 AGCTGATGTAGAGTCTATGATGAAAGCAGCTCTAGATAAATGGGGAACCAATAGATGTCT 626
Db 198 TGATGATGTTAAGCAATGATTTAAGAGTAGTTAGCCAAATTTGGTTCTTTAGATGTTT 257
QY 627 GGTAAATAATGCAAGGATTACAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTG 686
Db 258 AGTAATAATGCAAGGATTACTCGCATATTTTAAATGCGTATGAAAGCAAGAGTG 317
QY 687 GCAAGAGTTAATGATCTGATCTTACTGGCGTCTTCTTGTACACAGGCTGCAACAAA 746
Db 318 GGATGATGTTATTGACACAACTTAAAGGTGTATTAACTGCTATCATCTTCAAGGTCAGT 806
QY 747 AGTAATGATGAAAGAGAAAGGAAAAATTAACCAATTCGATCTGTAGTGTCTTAC 806
Db 378 ACAATGTTAAGACACAGTAGTGTGCTATCATCAATTTATCAAGTGTGTTGAGCAGT 437
QY 807 TGGCAATGTTGGCCAAAGTAAATTTATAGCCGACCAAGGCTGAGTGTGTTTCAAAA 866
Db 438 AGTAATTCGGGCAAGCAAACTATGTTGCAACAAAAGCAGGTTTATGTTGTTAACTAA 497
QY 867 AACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATCTATTGCAACAGGGTT 926
Db 498 ATCTGCGCGCGTGAATTAGCATCTCGTGTATCACTGTAAATGCACTTGCACCTGGTT 557
QY 927 CATTCATCTGATAGTATGCTCCGAACTTGGAGAGAGCTTGAAGAAATCTTGTCAAC 986
Db 558 TATTGTTCTGATATGACAGATGCTTTAAGGTGATGAGCTTAAAGAACAAATGTTGACTCA 617
QY 987 CATTCGCTGAGGAGATATGCGCAACAGAGAGATTTGCAAGGTTGTCAGTTTCTTGGC 1046
Db 618 AATTCCGTTAGCAGTTTGGTCAAGACACAGATATTGCTAATACAGTAGGTTCTTAGC 677
QY 1047 CCTTAAACCCCGAGTATATGATGAGTGGACAGGTCGTTACAAATTCACGAGGAGTGGT 1106
Db 678 ATCAGA---CAAGCAAAATATATACAGGTCNAACATCCATGTAATGCGTAATGTA 734
QY 1107 AATGTAA 1113
Db 735 CATGTAA 741
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RESULT 8

```
US-09-815-242-9002
; Sequence 9002, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9002
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(741)
US-09-815-242-9002
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Query Match      17.9%; Score 237.4; DB 9; Length 741;
Best Local Similarity 58.9%; Pred. No. 1.3e-48;
Matches 428; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 387 TGTGTGTTGTACAGGTCATCTAGAGGATTTGGTAAGGCAACTGCTCTAGCCCTTGAAA 446
Db 18 TGCTTTAGTAACAGGTGCATCAAGAGAAATGGACGTAGTATTGGTTACAATTAGCAG 77
QY 447 AGCAGATGCAAGGTTCTGTGTAATGATGCGGTCCTCGAAAGAGGCTGAAGAGTCTC 506
Db 78 AGAAGGATATAATGTAGCAGTAACTATGCGGCGCAAAAGAGAAAGCTGAAGCAGTAGT 137
QY 507 CAAAGAGATTGAAGCATCTGGTGCAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGA 566
Db 138 CGAAGAAATCAAAGCTTAAAGGTTGTGACAGTTTGGCATTTCAAGCAAAATGTCGGATGC 197
QY 567 AGCTGATGTAGAGTCTATGATGAAAGCAGCTCTAGATAAATGGGGAACCAATAGATGTCT 626
Db 198 TGATGATGTTAAGCAATGATTTAAGAGTAGTTAGCCAAATTTGGTTCTTTAGATGTTT 257
QY 627 GGTAAATAATGCAAGGATTACAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTG 686
Db 258 AGTAATAATGCAAGGATTACTCGCATATTTTAAATGCGTATGAAAGCAAGAGTG 317
QY 687 GCAAGAGTTAATGATCTGATCTTACTGGCGTCTTCTTGTACACAGGCTGCAACAAA 746
Db 318 GGATGATGTTATTGACACAACTTAAAGGTGTATTAACTGCTATCATCTTCAAGGTCAGT 806
QY 747 AGTAATGATGAAAGAGAAAGGAAAAATTAACCAATTCGATCTGTAGTGTCTTAC 806
Db 378 ACAATGTTAAGACACAGTAGTGTGCTATCATCAATTTATCAAGTGTGTTGAGCAGT 437
QY 807 TGGCAATGTTGGCCAAAGTAAATTTATAGCCGACCAAGGCTGAGTGTGTTTCAAAA 866
Db 438 AGTAATTCGGGCAAGCAAACTATGTTGCAACAAAAGCAGGTTTATGTTGTTAACTAA 497
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QY 867 AACAGTTGCCAGGAGTATCCAGCAGAAATATCAATGTGAATGCTATTGCACCAAGGTT 926
Db 498 ATCTGGGGCGCGTGAATTAGTACTCTCGTGTATCACTGTAAATGCAGTTGCACCTGGTTT 557
QY 927 CATTCGATCTGATGACTGCCGAACCTTGGAGAAGAGCTTGAGAAGAAATCTTGTCAAC 986
Db 558 TATTGTTTCTGATATGACAGATGCTTTAAGTGTAGCTTTAAGAACAAATGTTGACTCA 617
QY 987 CATTCGTTAGGAGATATGCCAACACAGAGGAGTTGCGAGGTTGGTGCAGTTCCTGGC 1046
Db 618 AATTCCGTTAGCAGCTTTTGGTCAAGACACAGATATTGCTTAATACAGTAGCGTTCTTAGC 677
QY 1047 CCTTAACCCGCGAGCTAGCTATATGATGACAGAGGTGCTTACAAATGACCGAGGAGTGGT 1106
Db 678 ATCAGA---CAAGCAAAATATATTACAGGTCAAAACAAATCCATGTAAATGGTGAATGTA 734
QY 1107 AATGTAA 1113
Db 735 CATGTAA 741

RESULT 9

US-09-815-242-4406
; Sequence 4406, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITEA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4406
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4406

Query Match 17.9%; Score 236.8; DB 9; Length 738;
Best Local Similarity 59.5%; Pred. No. 1.8e-48;
Matches 400; Conservative 0; Mismatches 272; Indels 0; Gaps 0;

QY 388 GTTGTGTTACAGTGTGATCTAGAGGATTCGTAAGGCAACTGCTTAGCCCTTGGAAA 447
Db 19 GCTTTAGTAACAGGTGTCATCAAGGAATTCGACTAGTATTGGCTTACAATTAGCAGAA 78
QY 448 CGAGATCAAGGTTCTGGTAACTATCCCGGTCTCGAAAGAGGCTGGAAGAGGTCTCC 507
Db 79 GAAGGATATATGTAGCAGTAACCTATCGAGGCAGCAAGAAAGCTGAGCAGTAGTC 138

QY 508 AAAGAGATTGAAGCATCTGTTGGTGGAGCTATCACTTCGGAGGAGATCTTTCAAGAA 567
Db 139 GAAGAAATCAAGCTAAAGGTGTTGACAGTTTGGGATTCAGCAAAATTTGCCGATGT 198
QY 568 GCTGATGTAGAGTCTATGATGAAGCAGCTCTAGATAAATGGGGAAACAATAGATGTGCTG 627
Db 199 GATGAAGTTAAGCAATGATTAAGAGTAGTTAGCCAATTTGGTCTTTAGATGTTTA 258
QY 628 GTAATAATGCGAGGATTAACAGAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGG 687
Db 259 GTAATAATGCGAGGATTAATCTCGGATAATTTATTAATCGTATGAAGAAACAAGAGTGG 318
QY 688 CAAGAGCTAATTTGATCTGAATCTTACTGGCGTCTTCTTTGTACACAGGCTGCAACAAA 747
Db 319 GACGATGTTTATGACACAAACTTAAAGGTGTATTTAATCTGATATCCAAAAGCAACCA 378
QY 748 GTAATGATGAAAAGAAAGGAAATTAATCAACATTTGATCTCTAGTGTGCTTACT 807
Db 379 CAAATGTTAAGACACAGTAGTGTGCTATCATCAATTTATCAAGTCTTGTGGAGCAGTA 438
QY 808 GGCATGTTGGCCAGCTAATTATAGCGCAGCCAGCGCTGGAGTGATTTGTTTCAAAA 867
Db 439 GGTAAATCCAGGACAGCAAACTATGTTGCAACAAAAGCAGGTGTTATTGTTTAACTAAA 498
QY 868 ACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGCACCAAGGTTTC 927
Db 499 TCTGGCGCGGTGAATTAGCACTCTGTTGTAICTGTTAAATGCGATTGCACTGTTT 558
QY 928 ATTGCATCTGATATGACTGCCGAACCTTGGAGAAGAGCTTGAGAAGAAATCTTTGCAACC 987
Db 559 ATTGTTTCTGATATGACAGATGCTTTAAGTGTAGCTTTAAAGAACAAATGTTGACTCAA 618
QY 988 ATTCCGTTAGGAGATATGCCAACACAGAGGAAGTTGCGAGGTTGTCGAGTTCCTGGCC 1047
Db 619 ATTCCGTTAGCAGCTTTTGTGTCAGACACAGATATTGCTTAATACAGTAGCGTTCTTAGCA 678
QY 1048 CTTAAACCCGCA 1059
Db 679 TCAGACAAAGCA 690

RESULT 10

US-09-974-300-6558
; Sequence 6558, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6558
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-6558

Query Match 16.0%; Score 212.8; DB 10; Length 744;
Best Local Similarity 56.9%; Pred. No. 1.6e-42;
Matches 410; Conservative 0; Mismatches 307; Indels 3; Gaps 1;

QY 391 GTTGTACAGGTGATCTAGAGGATTCGTAAGCAACTGCTTAGCCCTTGGAAAAGCA 450
Db 22 GTTGTACAGCGCTTCACGTGGAAATTGGCAAGCGATCGCCCTTGAACCTTGTGCCCCAAA 81

QY 787 GCATCTAGTGTCTTCTTACTGGCAATGTTGGCCAGCTAATTAATAGCGGAGCAAGGCT 846
Db 5181 TCATCAATTAATTTGGTCAAGCGGGGGAATTTGGTCAAAACAATCTACTCAGCTGCTAAAGCA 5240
QY 847 GGAGTGTATGTTTTCACAAAACAGTTGCCAGGAGATGCAAGCAGAAATATCAATGTG 906
Db 5241 GGTAGCTAGGATTCATTAATCATATTAGCTCTTGAATAGTACAGCGGTTACGGTT 5300
QY 907 AATGCTAATGACACAGGTTCAATGCTATGATGATGCTGCGAACTTGGAGAGAGCTT 966
Db 5301 AATGCAATTTGCCAGGATTTATTCAGAACGAAATGCTGATGCGAAATTCCTGAAGATGTT 5360
QY 967 GAGAGAGAAATCTTGTCAACATTCCTGTTAGGAGATATGCCAACAGAGAGATGCA 1026
Db 5361 CGTGCAAAAATGTTGGCAAAATTCACACTCGTCGCTTAGGTCAAGTGAAGAAATGCA 5420
QY 1027 GGGTGTGTCGAGTTCTCGGCCCTTAACCCCGCAGCTAGCTATATGACTGGACAGGTCCTT 1086
Db 5421 CGTGGAGTTGTTTACTTAGCAAAAGACGGCGC-----GTRCATTAAGGACACAGTTA 5474
QY 1087 ACAATGACGAGGATGTTGTAATGAAGATTG 1119
Db 5475 AACATTAACGCGGCTTATACATGTAATAAATG 5507

RESULT 14

US-09-479-040-8
; Sequence 8, Application US/09479040
; Publication No. US20020182690A1
; GENERAL INFORMATION:
; APPLICANT: McCool, Gabriel J.
; APPLICANT: Cannon, Maura C.
; APPLICANT: Cannon, Francis C.
; APPLICANT: Valentin, Henry E.
; APPLICANT: Gruys, Kenneth J.
; TITLE OF INVENTION: POLYHYDROXALKANOATE BIOSYNTHESIS ASSOCIATED PROTEINS
; FILE REFERENCE: N08212
; CURRENT APPLICATION NUMBER: US/09/479,040
; CURRENT FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Bacillus megaterium
US-09-479-040-8

Query Match 13.2%; Score 175.2; DB 10; Length 741;
Best Local Similarity 53.3%; Pred. No. 3.5e-33;
Matches 369; Conservative 0; Mismatches 323; Indels 0; Gaps 0;
QY 367 ACCAAGCTGGAAGCTCCAGTTGTTGTTACAGTGCATCTAGAGGAGTTGGTAAGGCA 426
Db 4 ACAACATTACAAGGTAAAGTAGCAATCGTACAGCGCGATCTAAAGTATCGGGGAGCA 63
QY 427 ACTGCTTAGCCCTTGGAAAGAGGATGCAAGTTCTGTGTAACATGATCCCGGCTCTCG 486
Db 64 ATTACAGTGTAGCTTCTTAATGGAGTAAAGTAGCAGTAAATATACAGCAGTAAA 123
QY 487 AAAGAGGCTGAAGAGTCTCCAAAGAGATTCAGCACTCTGTGTGGCTTATCACCTTC 546
Db 124 GAATCTGCAAGCAATTTGTAAGAAATTAAGACACCGCGGAGAGCTATTGGCGTT 183
QY 547 GGAGGAGATGTTTCAAAAGAGAGCTGATGTAGTCTATGATGAAGCAGCTCTAGATAAA 606
Db 184 CAAGCTGACGCTCTTATGTAGTACAGCAAAACACCTTAATCGAAGAACAAAAGCTGCG 243
QY 607 TGGGGAACAATAGATGCTGTTAAATATGAGGATTAACAGGACACATTTGTTGATG 666
Db 244 TTTGGTCAATTAGACATTTCTAGTAAACAATGCTGGAATTTACGCGGACCGTTTCAAG 303

QY 667 AGGATGAAGAAATCTCAGTGGCAGAGCTAATTAATGATCTGAATCTTACTGGCGTCTTCCT 726
Db 304 AAGTTAGGTGAAGAAATTTGAAAAAAGTAATTTGATGTAAACTTACATAGCGTATACAAC 363
QY 727 TGTACACAGCTGCAACAAAAAGTAATGATCAAAAAGAGAAAGGAAAAATTTATCAACATT 786
Db 364 ACAACATCAGCTCGCTTAACGACCTTTTAGAATCTGAGAGTGTGCTGTGTTATCAATATT 423
QY 787 GCATCTAGTGTGTTCTTACTGCGAAATGTTGGCCAAAGCTAATTTATAGCGCAGCAAGGCT 846
Db 424 TCATCAATTAATTTGTCAGCGGCGGATTTGGTCAAAACAATCTACTCAGCTGCTAAAGCA 483
QY 847 GGAGTGTATGTTTTCACAAAACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTG 906
Db 484 GGTATGCTAGGATTCATAATCATTAGCTCTTTGAACTAGTAAAGCAGCGTAAACGGTT 543
QY 907 AATGCTATTGACACAGGTTTCATTGTCATCTGATATGACTGCCGAACCTTGGAGAGAGCTT 966
Db 544 AATGCAATTTGCCAGGATTTATTGAACGGAATGTTGATGCAATTTCTGAAGATGTT 603
QY 967 GAGAGAAATCTTGTCAACCAATTCGTTAGGAGATATGGCCAAACAGAGGAGTTGCA 1026
Db 604 CGTGCAAAAATGTTGCGAAAATTCCAACTCGTCGCTTAGTTCACGCTGAAGAAATGCA 663
QY 1027 GGGTGTGTCGAGTTCTCGGCCCTTAACCCCGC 1058
Db 664 CGTGGAGTTGTTTACTTAGCAAAAGACGGCGC 695

RESULT 15

US-09-070-927A-458
; Sequence 458, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; Patrick J. Dillon
; Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 458:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6021 base pairs
; TYPE: nucleic acid

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i STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 458:
US-09-070-927A-458

Query Match      13.0%; Score 173; DB 10; Length 6021;
Best Local Similarity 54.6%; Pred. No. 4.1e-32;
Matches 397; Conservative 0; Mismatches 315; Indels 15; Gaps 2;

QY 388 GTTGTGTTACAGGTGCTAGAGGATGTTAAGGCACTGCTCTAGCCCTTGGAAAA 447
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 671 GTATTATTACTGGAAGCACTCGTGGGATGTTAAGCAGTTGCGTAGCTTTTCGAAA 730
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 448 GCAGATCCAGGTTCTGGTAAACTATGCCCGCTCTCGAAGAGGCTGAAGAGTCTCC 507
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 731 GAGCGGCCCAATATTGTCTTAAACGGTCGGAGTGAGATTA-----CGCCAGAACACGA 784
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 508 AAAGAGATTGAAGCATCTGGTGGTGAAGCTATCACCTTCGGAGGAGATGTTTCAAAAGAA 567
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 785 CAGGAATTGAAGCCTTTGGGTAAATCTATTGGCCTTCTGGAGATATTCCGATTTT 844
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 568 GCTGATGAGAGTCTATGATGAAAGCAGCTCTAGATAAATGGGGAACAAATAGATGCTG 627
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 845 GATCGGCGAGGTGAGATGTTCAAGCAACAGTTGACCAATTAGGCTCGATTGATATTCTG 904
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 628 GTAAATAATGAGGGATTACACAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGG 687
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 905 GTGAATAACCTGGGATTACGANTGACAAATTAATTATTACGAATGACAAAAGAGGATTT 964
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 688 CAAGACGTAAATTGATCTGAATCTTACTGGCGTCTTCCTTTGACACAGGCTGCAACAAA 747
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 965 AATGCTGTTAGATATTAACTTTGTTAGGAACCTTTTAACTGACCCAGCAGCGGTTAAA 1024
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 748 GTAATGATGAAAAAGAGAAAGGAAAAATTATCAACATTGCAATCTGTATGTTGGTCTTACT 807
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1025 CGTATGATGAACAACGAAGTGGTGGATTATTAATATGGCTVAGCGTTTCTGGTTTAATG 1084
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 808 GGCATGTTGGCCAGCTAAATTATAGCCAGCCAGGCTGGAGTGATTTGGTTTCACAAA 867
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1085 GGAATGTTGGTCAAGCAAACTACGCTGCGAGTAAAGCGGTTGCTGGTTGTTTACTAAA 1144
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 868 ACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGCACAGGGTTC 927
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1145 TCGGTGGCAGAGAGTTGGCGCGCGGTATTACCTGCAATGCGATTGCACCAGGGTTT 1204
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 928 ATTGCATCTGATATGACTGCCGAACTTGGAGAGAGCTTTGAGAGAAAATCTTGTCAACC 987
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1205 ATCCAAACAGAAATGACGAGTGTTTTATCGGAAAAAGTTAAAAACACAAATGAATCGCAA 1264
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 988 ATTCGGTTAGGAGATATGCCAACAGAGGAAGTTGCAGGGTTGGTCGAGTTCTCGGCC 1047
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1265 ATTCCTTTACAAACGTTTGGGCAAGTCGAAGATGTCGAGCTACAGCGATTTTCTTAGCT 1324
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1048 CTTAACCCCGCAGCTAGCTATATGCTGACAGAGGTGCTTTACAAATTGACGGAGGATGGTA 1107
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1325 AAAAGTCC-----CTATATTACTGGGCAAGTCGTCAATGTCGATGCGCGGCTTACTC 1375
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1108 ATGTAAG 1114
Db  ||| ||| |||
QY 1376 ATGCACG 1382
Db  ||| ||| |||
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Search completed: November 7, 2003, 17:10:27
Job time : 450 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 13:17:29 ; Search time 3088 Seconds
(without alignments)

10436.443 Million cell updates/sec

Title: US-10-024-806-1

Perfect score: 1326

Sequence: 1 G9CGGAGCTTCCAAAGCC.....aaaaaaaaaaaaaaaaaaaa 1326

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562794

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.*

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1326	100.0	1342	11 AY106146	AY106146 Zea mays
2	635	47.9	646	14 CB604782	CB604782 3529.1.61
3	615.2	46.4	639	13 BQ744718	BQ744718 946108E11
4	606	45.7	659	14 CD484893	CD484893 3529.1.11

C	5	598.4	45.1	600	10	BE510479
	6	598.4	45.1	648	13	BU098345
	7	585.6	44.2	626	10	BE510480
	8	584.6	44.1	637	13	BQ778788
C	9	583.4	44.0	624	13	BQ778787
	10	576.2	43.5	618	13	BQ779235
	11	570.4	43.0	600	13	BQ293972
	12	550	41.5	557	13	BU092521
C	13	545.8	41.2	589	12	BM737475
	14	538.2	40.6	577	14	CA830470
	15	533.8	40.3	539	13	BU092794
C	16	525.2	39.6	560	13	BU050646
	17	524.8	39.6	530	13	BO667989
	18	511	38.5	553	12	BF543006
C	19	502.2	37.9	578	14	CB604576
	20	493.2	37.2	532	12	BM737474
C	21	491.2	37.0	525	12	BI542734
	22	483.6	36.5	490	12	BM953553
C	23	457	34.5	457	14	CD510389
	24	456.8	34.4	623	9	AV938005
	25	439.6	33.2	692	10	BF473272
	26	438	33.0	679	14	CB972131
C	27	437.6	33.0	640	9	AV913625
	28	429.6	32.4	692	9	AV943057
	29	426.6	32.2	852	12	BM814438
	30	426.4	32.2	754	12	BM408233
	31	419.8	31.7	765	12	BM814281
	32	419.6	31.6	547	12	BM097231
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C	41	380.6	28.7	677	9	AI622760
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ALIGNMENTS

RESULT 1	AY106146	AY106146	1342 bp	mrna	linear	HTC 16-OCT-2002
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DEFINITION	AY106146	Zea mays	PC0074795	mrna	sequence.	
ACCESSION	AY106146	Zea mays	PC0074795	mrna	sequence.	
VERSION	AY106146.1	GI:21209224				
KEYWORDS	HTC					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE	1 (bases 1 to 1342)					
AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 1342)					
AUTHORS	Coe, E.H.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA					
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org, or NCBI, www.ncbi.nlm.nih.gov. When the source of the					

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
Clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1342)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes

Unpublished (2002)
2 (bases 1 to 1342)
Coe, E.H.

Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org, or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

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  Location/Qualifiers
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ORIGIN				

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Best Local Similarity	100.0%;	Pred. NO. 2.2e-126;		
Matches 1326;	Conservative 0;	Mismatches 0;	Indels 0;	

[illegible]

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Db	797	AACATTGCATCTGTAGTTGGTCTTACTTGGCAATGTTGGCCAAAGCTAATTATAGCGCAGCC	856
Qy	841	AAGCGTGGAGTGAATGGTTTTCACAAAACAGTTGCCAGGAGATGCAACAGCAAAATATC	900
Db	857	AAGCTGGAGTGATTTGGTTTTCACAAAACAGTTGCCAGGAGATGCAACAGCAAAATATC	916
Qy	901	AATGTGAATGCTATTTGCACACAGGGTTCAATTGCAATCTGATATGACTGCCGAATTTGGAGAA	960
Db	917	AATGTGAATGCTATTTGCACACAGGGTTCAATTGCAATCTGATATGACTGCCGAATTTGGAGAA	976
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Qy	1021	GTTGCAGGTTGTTGAGTTTCTTGGCCCTTAAACCCCGCAGCTAGCTATATGACTGGACAG	1080
Db	1037	GTTGCAGGTTGTTGAGTTTCTTGGCCCTTAAACCCCGCAGCTAGCTATATGACTGGACAG	1096
Qy	1081	GTGCTTACAATTCAGCGGAGGATGTAAGTAAGATTTGAGTTAGCTTGATGCATTTCTA	1140
Db	1097	GTGCTTACAATTCAGCGGAGGATGTAAGTAAGATTTGAGTTAGCTTGATGCATTTCTA	1156
Qy	1141	CTTTTGTCTGAGCATTTAAATGCTGAAACACCTTCTGTGCAACGGCGGATTTTGACACAA	1200
Db	1157	CTTTTGTCTGAGCATTTAAATGCTGAAACACCTTGTGCAACGGCGGATTTTGACACAA	1216
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Db	1337	AAAAAA 1342	

RESULT 2
CB604782

LOCUS

DEFINITION

11

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANIS

1

REFERENCE

AUTHORS

TITLE

FORM 1041

**JOURNAL
COMMENT**

COMMENT

FEATURES

SOUTHERN

303


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/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake labs"
/note="Organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu amplified. Ampicillin is the selection marker."
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ORIGIN
Query Match 47.9%; Score 635; DB 14; Length 546;
Best Local Similarity 99.8%; Pred. No. 5.8e-56;
Matches 646; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 24 TCCGCCAATAGACTCTCCCATCGTCTCTGCTCCGTCACGGCTCAAAATACCTCCGCT 83
Db 1 TCCGCCAATAGACTCTCCCATCGG-GCTTGTCTCCGTCACGGCTCAAAATACCTCCGCT 59
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Qy 144 CCGAGCGCCCTCATGGCCACGCGCGCGCCGACCGCAGCAGCAGCAGCAGCTCTCTCCC 203
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Qy 204 GGCTGCGGCTGGAGCAGCGCGCGCGCGCGCTCCGCGCGCGGTTTCGTCAGCTTGG 263
Db 180 GGCTGCGGCTGGAGCAGCGCGCGCGCGCGCTCCGCGCGCGGTTTCGTCAGCTTGG 239
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Db 300 AACCAGTGTCTGCTGTTGAAACAGCAGTGTGTAAGGATGTTAAAGATGCTACCAAGCTGGA 359
Qy 384 AGTTGTTGTTTACAGTGTGATCTAGAGGATGTTGTAAGGATGTTGTAAGGATGTTGTAAG 443
Db 360 AGTTGTTGTTTACAGTGTGATCTAGAGGATGTTGTAAGGATGTTGTAAGGATGTTGTAAG 419
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Db 480 CTCCAAAGAGATGAGCAGTCTGTTGAGGCTATCACCCTCGGAGGAGATGTTCAA 539
Qy 564 AGAAGCTGATGTAGAGTCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGT 623
Db 540 AGAAGCTGATGTAGAGTCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGT 599
Qy 624 GCTGTAATAATGAGGATGATACGAGACACATTTGTTGATGAGA 670
Db 600 GCTGTAATAATGAGGATGATACGAGACACATTTGTTGATGAGA 646

RESULT 3
BQ744718 639 bp mRNA linear EST 17-JUL-2002
LOCUS 946108E11.v1 946 - tassels primordium prepared by Schmidt lab Zea
DEFINITION mays cDNA, mRNA sequence.
ACCESSION BQ744718
KEYWORDS BQ744718.1 GI:21891505
SOURCE Zea mays
ORGANISM Zea mays

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

Maize ESTs from various cDNA libraries sequenced at Stanford University

Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946108 row: E column: 11.
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/clone_lib="946 - tassels primordium prepared by Schmidt lab"
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BASE COUNT 168 a 138 c 180 g 153 t

Query Match 46.4%; Score 615.2; DB 13; Length 639;
Best Local Similarity 99.5%; Pred. No. 5.8e-54;
Matches 617; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 220 GCGGGGCGCGCGCGCTCCCGCGGGGTTCTCACGTTTGTGGAGCGCGCGCGC 279
Db 20 GCGGGGCGCGCGCGCTCCCGCGGGGTTCTCACGTTTGTGGAGCGCGCGCGC 79
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Qy 340 GTTGAACAAGCAGTTGTAAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 399
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Qy 400 GGTGATCTAGAGGATGTTGTAAGGCAACTGCTTAGCCCTTGAAGAGGATGCAAG 459
Db 200 GGTGATCTAGAGGATGTTGTAAGGCAACTGCTTAGCCCTTGAAGAGGATGCAAG 259
Qy 460 GTTCTGTGTAACACTATGCGCGTCTCGAAGAGCTCAAGAGGCTCCCAAGAGATTGAA 519
Db 260 GTTCTGTGTAACACTATGCGCGTCTCGAAGAGCTCAAGAGGCTCCCAAGAGATTGAA 319
Qy 520 GCATCTGCTGTGAGGCTTATCACCTTCGGAGGAGATGTTTCAAAGAGCTGTAGAG 579
Db 320 GCATCTGCTGTGAGGCTTATCACCTTCGGAGGAGATGTTTCAAAGAGCTGTAGAG 379
Qy 580 TCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGCTGCTGTAATAATGCA 639
Db 380 TCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGCTGCTGTAATAATGCA 439
Qy 640 GGGATTAACAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGCAGAGAGCTAAT 699
Db 440 GGGATTAACAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGCAGAGAGCTAAT 499
Qy 700 GATCTGAATCTTACTGGCGCTCTTCTTGTGTACACAGGCTGCACAAAGATGATGAA 759

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Db      500  GATCTGAATCTTACTGGTGTCTTCCTCTGTACACAGGCTGCACAAAGTATGANGAAA 559
Qy      760  AAGAGAAAGGAAATAATATCAACATTCGATCTGTAGTGTGTTCTTACTGGCAATGTTGGC 819
Db      560  AAGAGAAAGGAAATAATATCAACATTCGATCTGTAGTGTGTTCTTACTGGCAATGTTGGC 619
Qy      820  CAAGCTAATTATAGCGCAGC 839
Db      620  CAAGCTAATTATAGCGCAGC 639

RESULT 4
LOCUS   CD484893
DEFINITION 3529_1_110_1_C12.x.1 3529 - 2 mm ear tissue from Schmidt and Hake
VERSION  CD484893
KEYWORDS  CD484893.1 GI:31406161
SOURCE   EST.
ORGANISM Zea mays
          Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
          1 (bases 1 to 659)
REFERENCE Walbot,V.
AUTHORS   Maize ESTs from various cDNA libraries sequenced at Stanford
TITLE     Unpublished
JOURNAL   Department of Biological Sciences
COMMENT   Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
          Plate: 3529_1_110_1 row: C column: 12.

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        Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu
        amplified. Ampicillin is the selection marker."

BASE COUNT  183 a 169 c 116 g 191 t
ORIGIN
Query Match      45.7%; Score 606; DB 14; Length 659;
Best Local Similarity 98.5%; Pred. No. 4.9e-53;
Matches 654; Conservative 0; Mismatches 5; Indels 5; Gaps 4;

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Db      659  GCTGATGTAGAGTCTATGATGAAGCAGCTCTAGATAAATGGGAACAATAGATGTGCTG 600
Qy      628  GTAATAATGCGGATTAACGAGACACATTTGATGAGATGAAGAAATCTCAGTGG 687
Db      599  GTAATAATGCGGATTAACCGAGACCATCTGATGAAGATGAAGAAATCTCAGTGG 540
Qy      688  CAAGACGTAATTGATCTGATCTTACTGGCGCTTCTCTTTGATACAGCGCTGCACAAAA 747
Db      539  CAAGACGTAATTGATCTGATCTTACTGGCGCTTCTCTTTGATACAGCGCTGCACAAAA 480
Qy      748  GTAATGATGAAGAAAGGAAATAATATCAACATTCGATCTGTAGTGTGTTCTTACT 807

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Db      479  GTAATGATGAAGAAAGGAAATAATATCAACATTCGATCTGTAGTGTGTTCTTACT 420
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Db      419  GGCAATGTTGCCCAAGCTAATATTAGCGCAGCCAAAGCTGGAGTGAATGGTTTTCACAAAA 360
Qy      868  ACAGTTCGCCAGGAGATGCAAGCAGAAATATCAATGTGAATGCTATTGCACAGGGTTC 927
Db      359  ACAGTTCGCCAGGAGATGCAAGCAGAAATATCAATGTGAATGCTATTGCACAGGGTTC 300
Qy      928  ATTGCATCTGATATGACTGCCGAACCTTGGAGAGAGAGCTTGGAGAGAAATCTTCTCAACC 987
Db      299  ATTGCATCTGATATGACTGCCGAACCTTGGAGAGAGAGCTTGGAGAGAAATCTTCTCAACC 240
Qy      988  ATTCCGTTAGGAGATATGCCCAACCCAGAGAGAGTTGCAGGGTTGGTGCAGTTCTCTGGCC 1047
Db      239  ATTCCGTTAGGAGATATGCCCAACCCAGAGAGAGTTGCAGGGTTGGTGCAGTTCTCTGGCC 180
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Db      179  CTTAAACCCCGCAGCTAGCTATATGACTGGACAGGTGCTTACATTTGACGGAGGATGGTA 120
Qy      1108  ATGTAAGATTTGAGTTAGCTTGCACCTTCTACTTTTGTGAGCATTTAATGTTGAACA 1167
Db      119  ATGTAAGATTTGAGTTAGCTTGCACCTTCTACTTTTGTGAGCATTTAATGTTGAACA 62
Qy      1168  CCTTGTGTGTCACGGCGGATTTTGGACAAATTAATGATGTGTCTCTTTTGTGAATA 1227
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Qy      1228  CTCT 1231
Db      4  CTCT 1

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DEFINITION 946053B11.x1 946 - tassell primordium prepared by Schmidt lab Zea
          mays cDNA, mRNA sequence.
ACCESSION BE510479
VERSION   BE510479.1 GI:9731727
KEYWORDS  EST.
SOURCE   Zea mays
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          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
          1 (bases 1 to 600)
REFERENCE Walbot,V.
AUTHORS   Maize ESTs from various cDNA libraries sequenced at Stanford
TITLE     Unpublished
JOURNAL   Department of Biological Sciences
COMMENT   Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
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DEFINITION BE510480 626 bp mRNA linear EST 07-AUG-2000
mays cDNA, mRNA sequence.
ACCESSION BE510480
VERSION BE510480.1 GI:9731728
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 626)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL Unpublished
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 725 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946053 row: B column: 11.
FEATURES
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lab"
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Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybridZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."
BASE COUNT 136 a 169 c 175 g 146 t
ORIGIN
Query Match 44.2%; Score 585.6; DB 10; Length 626;
Best Local Similarity 97.6%; Pred. No. 6e-51; Indels 6; Gaps 2;
Matches 617; Conservative 0; Mismatches 9;
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DB 1 TGTCTCCCTCTGGCTTCCGCGCTCTCTTCGGCTCCTTCGCGTCCCGAGCCCGCTCATGG 60
QY 161 CCACCGCGCGCGCCACCGAGACAGACAGAGTCTCTCCCGCTCGCGTGGAGAGCAG 220
DB 61 CCACCGCGCGCGCCACC---GTAGCAGCAGCAGTCTCTCCCGCTGCC---CACGCG 114
QY 221 CCGGGCGCGCGCGCGCTCCGCGCGGGTTCGTACGTTGGTGGAGCGCGCGCGCT 280
DB 115 CCGGGCGCGCGCGCGCGCTCCGCGCGGGGTTGGTACGTTGGTGGAGCGCGCGCGCT 174
QY 281 TCTCTCCCAACGCTGCGGTCGCGCGCTCTCTGGTGTGCAACCCCATGTTGCTGCTG 340
DB 175 TCTCTCCCAACGCTGCGGTCGCGCGCTCTCTGGTGTGCAACCCCATGTTGCGCTG 234
QY 341 TTGAACAAGAGCTTTGTAAGAAGATGTACCAAGCTGGAAGCTCCAGTTGTTGTTACAG 400
DB 235 TTGAACAAGCAATTGTAAGAAGATGTACCAAGCTGGAAGCTCCAGTTGTTGTTACAG 294
QY 401 GTGCATCTAGAGGGATTGGTAGGCACTGCTCTAGCCCTTGGAAAAGCAGGATCAAGG 460

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Db 295 GTGCATCTAGAGGGATTGGTAAGGCACTGCTCTAGCCCTTGGAAAAGCAGGATCAAGG 354
QY 461 TTCTGTGTAACATATGCCCGGTCTCGAAAAGAGGCTGAAGAGGTCTCCAAAAGAGATTGAAG 520
DB 355 TTCTGTGTAACATATGCCCGGTCTCGAAAAGAGGCTGAAGAGGTCTCCAAAAGAGATTGAAG 414
QY 521 CATCTGTGTGAGGTATACACCTTCGGAGGAGATGTTTCAAAGAAGCTGATGTAGAT 580
DB 415 CATCTGTGTGAGGTATACACCTTCGGAGGAGATGTTTCAAAGAAGCTGATGTAGAT 474
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DB 595 ATCTGAATCTTACTGGTGTCTTCTCTTTGTACA 626

RESULT 8
BQ778788
LOCUS
DEFINITION BQ778788 637 bp mRNA linear EST 26-JUL-2002
mays cDNA, mRNA sequence.
ACCESSION BQ778788
VERSION BQ778788.1 GI:21987260
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 637)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL Unpublished
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946114 row: C column: 11.
FEATURES
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inflorescence development"
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lab"
/note="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI;
Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybridZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."
BASE COUNT 140 a 177 c 177 g 143 t
ORIGIN
Query Match 44.1%; Score 584.6; DB 13; Length 637;
Best Local Similarity 97.5%; Pred. No. 7.5e-51;
Matches 627; Conservative 0; Mismatches 9; Indels 7; Gaps 3;

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Db 1 TACTCCGCTGCATCTCC--AAGACACATGCTCCCTCTGGCTCCCGGCTCTCTCGGCT 59
QY 134 CTTTGGGCTCCGACGCGCCCTCATGCGCCACCGCGCGCGCGCGCGCGCGCGCGCGCG 193
Db 60 CTTTGGGCTCCGACGCGCCCTCATGCGCCACCGCGCGCGCGCGCGCGCGCGCGCGCG 116
QY 194 TCTCTCTCCGCGCTGCGGTGGAGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 253
Db 117 TCTCTCTCCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 173
QY 254 TCAGTTTGGTGGAGGCGCGCGCGCTCTCTCCACGCTGCGGTCCGCGCGCGGTGTTCT 313
Db 174 TCAGTTTGGTGGAGGCGCGCGCGCTCTCTCTCCACGCTGCGGTCCGCGCGCGGTGTTCT 233
QY 314 CTGTGTGCAAAACCATGTTGCTGCTGTTGAACAGCAGTTGTAAGAGATGCTACCAAGC 373
Db 234 CTGTGTGCAAAACCATGTTGCTGCTGTTGAACAGCAGTTGTAAGAGATGCTACCAAGC 293
QY 374 TGGAGTCCAGTTGTTGTTGTTTACAGTGTCATCTAGAGGATGGTAAGCACTGCTC 433
Db 294 TGGAGTCCAGTTGTTGTTGTTTACAGTGTCATCTAGAGGATGGTAAGCACTGCTC 353
QY 434 TAGCCCTTGGAAAGCAGGATGCAAGGTTCTGTTAAACTATGCCCGTCTCGAAAGAGG 493
Db 354 TAGCCCTTGGAAAGCAGGATGCAAGGTTCTGTTAAACTATGCCCGTCTCGAAAGAGG 413
QY 494 CTGAAGAGGCTCTCAAAGAGATGAAGCATCTGGTGGTGGGCTATCACCTTCGAGAGG 553
Db 414 CTGAAGAGGCTCTCAAAGAGATGAAGCATCTGGGCGTGGGCTATCACCTTCGAGAGG 473
QY 554 ATGTTTCAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 613
Db 474 ATGTTTCAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 533
QY 614 CAATAGATGCTGCTGTAATTAATGATGATGATGATGATGATGATGATGATGATGATG 673
Db 534 CAATAGATGCTGCTGTAATTAATGATGATGATGATGATGATGATGATGATGATGATG 593
QY 674 AGAATCTCAGTGGCAAGACGTAATGATGATGATGATGATGATGATGATGATGATG 716
Db 594 AGAATCTCAGTGGCAAGACGTAATGATGATGATGATGATGATGATGATGATGATG 636
```

RESULT 9

BQ778787/c

LOCUS

DEFINITION BQ778787 624 bp mRNA linear EST 26-JUL-2002
946114C11.x1 946 - tassell primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.

ACCESSION

VERSION

BQ778787.1

GI:21987259

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

REFERENCE

AUTHORS

Walbot,V.

TITLE

Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL

COMMENT

Unpublished

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 946114 row: C column: 11.

Location/Qualifiers

source

1. 624

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="OH43"

/db_xref="taxon:4577"

/tissue type="tassels"

/dev stage="just after the transition from vegetative to

inflorescence development"

/lab_host="XLOLR"

/clone_lib="946 - tassell primordium prepared by Schmidt

lab"

/notes="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;

Site 2: XhoI; George Chuck dissected immature tassels

between 1mm and 3mm. Sharon Stanfield prepared the cDNA

library in HybriZAP. Sample insert size range was 350 bp

to 3 Kb with a 1 Kb average."

BASE COUNT 175 a 153 c 121 g 175 t

ORIGIN

Query Match 44.0%; Score 583.4; DB 13; Length 624;

Best Local Similarity 97.3%; Pred. No. 1e-50;

Matches 604; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 682 CAGTGGCAAGACGCTAATGATCTGAATCTTACTGGGCTCTTCTTGTACACAGGCTGCA 741

Db 624 CAGTGGCAAGACGCTAATGATCTGAATCTTACTGGTGTCTTCTTGTACCCAGGCTGCA 565

QY 742 ACAAAGTATGATGAAAAAGAGAAAGGAAAAATATCAACATTTGATCTGTAGTTGGT 801

Db 564 ACAAAGTATGATGAAAAAGAGAAAGGAAAAATATCAACATTTGATCTGTAGTTGGT 505

QY 802 CTTACTGGCAATCTGGCCAGCTAATATAGCGCAGCAGGCTGGAGTGGTTTC 861

Db 504 CTTACTGGCAATCTGGCCAGCTAATATAGCGCAGCAGGCTGGAGTGGTTTC 445

QY 862 ACAAACAGTTCGCCAGGAGTATCAAGCAGAAATATCAATGTGAATGCTATTGCACCA 921

Db 444 ACAAACAGTTCGCCAGGAGTATCAAGCAGAAATATCAATGTGAATGCTATTGCACCA 385

QY 922 GGTTTCATTCATCTGATATGACTGCGAACTTTGGAGAGAGCTTGAGAAAGAAATCTTG 981

Db 384 GGTTTCATTCATCTGATATGACTGCGAACTTTGGAGAGAGCTTGAGAAAGAAATCTTG 325

QY 982 TCAACCATTCCTGTAGGAGATATGCCACAGAGAGAGCTTCAGGGTTGTCGAGTTC 1041

Db 324 TCAACCATTCCTGTAGGAGATATGCCACAGAGAGAGCTTCAGGGTTGTCGAGTTC 265

QY 1042 CTGGCCCTTAAACCCCGCAGCTATATGACTGGACAGGCTGTACAAATTCAGCGAGGG 1101

Db 264 CTGGCCCTTAAACCCCGCAGCTATATGACTGGACAGGCTGTACAAATTCAGCGAGGG 205

QY 1102 ATGGTAATGTAAGATTGAGTTAGTTAGTGTGATGCTTCTACTTTTGTGAGCAATTAATG 1161

Db 204 ATGGTAATGTAAGATTGAGTTAGTTAGTGTGATGCTTCTACTTTTGTGAGCAATTAATG 145

QY 1162 TGAACACCTCTGTGTGTCAGCGGCGATTTTGGACAAATATAGTGTCTCTCTCTTT 1221

Db 144 TGAACACCTCTGTGTGTCAGCGGCGATTTTGGACAAATATAGTGTCTCTCTCTTT 85

QY 1222 GTAATCTCTCTGTAATAATCTAG-CATGTGGAATGGAAGTTGAAATCTGGGTTTTCG 1280

Db 84 GTAATCTCTCTGTAATAATCTAGCCATGTGAATGGAAGTTGAAATCTGGGTTTTCG 25

QY 1281 TGTAAAAAATAAAAAAATAAAAAA 1301

Db 24 TGTAAAAAATAAAAAAATAAAAAA 4

RESULT 10

BQ779235

LOCUS

DEFINITION BQ779235 618 bp mRNA linear EST 26-JUL-2002

946117H09.v1 946 - tassell primordium prepared by Schmidt lab Zea

mays cDNA, mRNA sequence.

FEATURES

```

ACCESSION BQ779235
VERSION BQ779235.1 GI:21987707
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 618)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL Unpublished
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946117 row: H column: 09.
FEATURES
source
1..618
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="XLOLR"
/clone_lib="946 - tassels primordium prepared by Schmidt
lab"
/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."
BASE COUNT 180 a 108 c 159 g 170 t 1 others
ORIGIN
Query Match 43.5%; Score 576.2; DB 13; Length 618;
Best Local Similarity 99.0%; Pred. No. 5.5e-50; Indels 2; Gaps 2;
Matches 600; Conservative 0; Mismatches 4;
657 ATTGTTGATGAGGATGAAGAATCTCAGTGGCAAGCGTAATTGATCTGAATCTTACTGG 716
15 ACTGTTGATGAGGATGAAGAATCTCAG-GGCNAGACGTAATTGATCTGAATCTTACTGG 73
717 CGTCTTCCTTTGTACACAGGCTGCACAAAAGTAATGATGAAGAAGAGAAAGGAAAAAT 776
74 -GTCTTCCTTTGTACACAGGCTGCACAAAAGTAATGATGAAGAAGAGAAAGGAAAAAT 132
777 TATCAACATTGTCATCTGATGTTGGTCTTACTGGCAATGTCGCCAAGCTAATTATAGCGC 836
133 TATCAACATTGTCATCTGATGTTGGTCTTACTGGCAATGTTGCCNAGTAATTATAGCGC 192
837 AGCCAAGGCTGGAGTGATGTTGTTTCACAAAACAGTTCCGAGGGAGTATGCAAGCAGAAA 896
193 AGCCAAGGCTGGAGTGATGTTGTTTCACAAAACAGTTCCGAGGGAGTATGCAAGCAGAAA 252
897 TATCAATGTGAATGCTATTGCAACAGGGTTCATTCATCTGATATGACTGCGCAACTGG 956
253 TATCAATGTGAATGCTATTGCAACAGGGTTCATTCATCTGATATGACTGCGCAACTGG 312
957 AGAAGAGCTTGAGAGAAAATCTTCTCAACCAATTCGTTAGGAGATATGCCAACACAGA 1016
313 AGAAGAGCTTGAGAGAAAATCTTGTCAACCAATTCGTTAGGAGATATGCCAACACAGA 372
1017 GGAAGTTGAGGCTTGGTCGAGTTCCTTGGCCCTTAACCCCGCAGCTAGCTATATGACTGG 1076
373 GGAAGTTGAGGCTTGGTCGAGTTCCTTGGCCCTTAACCCCGCAGCTAGCTATATGACTGG 432

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QY 1077 ACAGGTGCTTACAATTGACGGGGGATGCTAATGTAAGATTTGAGTTAGCTTGAATGCACT 1136
DB 433 ACAGGTGCTTACAATTGACGGGGGATGCTAATGTAAGATTTGAGTTAGCTTGAATGCACT 492
QY 1137 TCTACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTGTCACGGGCGAATTTTGACA 1196
DB 493 TCTACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTGTCACGGGCGAATTTTGACA 552
QY 1197 ACAAAATAGTGTCTCTCTTTCTTTCTTAATATCTCTCTGTAATAAATCTAGCATGTGGAA 1256
DB 553 ACAAAATAGTGTCTCTCTTTCTTTCTTTGGAATACTCTCTGGAATAAATCTAGCATGTGGAA 612
QY 1257 TCGAAG 1262
DB 613 TCGAAG 618
RESULT 11
BQ293972
LOCUS BQ293972
DEFINITION 1091024E01.y3 1091 - Immature ear with common ESTs screened by
Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION BQ293972 GI:20802922
VERSION BQ293972
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 600)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL Unpublished
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1091024 row: E column: 01.
FEATURES
source
1..600
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="Inflorescence meristem - floral organ
primordia"
/dev_stage="0.5 cm to 2 cm"
/lab_host="Stratagene XLOLR"
/clone_lib="1091 - Immature ear with common ESTs screened
by Schmidt lab"
/note="Organ: Immature ear; Vector: PAD-GAL4; Site 1:
EcoRI; Site 2: XhoI; RNA from library 606 was filtered for
common ESTs found in 606."
BASE COUNT 186 a 104 c 144 g 166 t
ORIGIN
Query Match 43.0%; Score 570.4; DB 13; Length 600;
Best Local Similarity 99.8%; Pred. No. 2.2e-49; Indels 0; Gaps 0;
Matches 571; Conservative 0; Mismatches 1;
697 ATTGATCTGAATCTTACTGGCGTCTTCTTTGTACACAGGCTGCAACAAAAGTAATGATG 756
DB 1 ATTGATCTGAATCTTACTTGTGTTCTTCTTTGTACACAGGCTGCAACAAAAGTAATGATG 60
QY 757 AAAAAGAGAAAGGAAAAAATATCAACATTGCTAGTCTTCTTCTTCTTCTTCTTCTTCTT 816
DB 61 AAAAAGAGAAAGGAAAAAATATCAACATTGCTAGTCTTCTTCTTCTTCTTCTTCTTCTT 120

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817 GGCCAGCTAATTATAGCGCAGCAGCGCTGGAGTGATGGTTTTCACAAAACAGTTGCC 876
 Db |||||
 121 GGCCAGCTAATTATAGCGCAGCAGCAGCTGGAGTGATGGTTTTCACAAAACAGTTGCC 180
 Qy |||||
 877 AGGAGTATGCAACGAGAAATATCAATGTGAATGCTATTGCACAGGTTTCATTGCACT 936
 Db |||||
 181 AGGAGTATGCAACGAGAAATATCAATGTGAATGCTATTGCACAGGTTTCATTGCACT 240
 Qy |||||
 937 GATATGCTCGCGAATCTTGAGAGAGAGCTTGAGAGAAATCTTGTCACCAATCCGTTA 996
 Db |||||
 241 GATATGCTCGCGAATCTTGAGAGAGAGCTTGAGAGAAATCTTGTCACCAATCCGTTA 300
 Qy |||||
 997 GGGAGATATGCCAACAGAGAGAGTTGCAGGTTGTCAGATTCCTGGCCCTTAACCCC 1056
 Db |||||
 301 GGGAGATATGCCAACAGAGAGAGTTGCAGGTTGTCAGATTCCTGGCCCTTAACCCC 360
 Qy |||||
 1057 GCAGTAGCTATATGACTGACAGAGTCTTACAATTTGACGAGGAGTGAATGTAAGAT 1116
 Db |||||
 361 GCAGTAGCTATATGACTGACAGAGTCTTACAATTTGACGAGGAGTGAATGTAAGAT 420
 Qy |||||
 1117 TTGATGAGCTTGATGCACTTCTACTTTGCTGAGCAATTTAATGTTGAAACACCTTGTTG 1176
 Db |||||
 421 TTGATGAGCTTGATGCACTTCTACTTTGCTGAGCAATTTAATGTTGAAACACCTTGTTG 480
 Qy |||||
 1177 TGCAAGGCGGATTTTGACACAAATAGTCTTCTCTTTCTTTTGTAACTCTCTGCT 1236
 Db |||||
 481 TGCAAGGCGGATTTTGACACAAATAGTCTTCTCTTTCTTTTGTAACTCTCTGCT 1296
 Qy |||||
 1237 AATAAATCTAGCATGTGGAATGGAATTTGAAA 1268
 Db |||||
 541 AATAAATCTAGCATGTGGAATGGAATTTGAAA 572

RESULT 12

BU092521 557 bp mRNA linear EST 29-AUG-2002
 LOCUS 946152D04.y1.946 - tassal primordium prepared by Schmidt lab Zea
 DEFINITION mays cDNA, mRNA sequence.

ACCESSION BU092521

VERSION BU092521.1 GI:22542083

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 557)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL University

COMMENT Unpublished

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 946152 row: D column: 04.

FEATURES

source

1. .557

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="OH43"

/db_xref="taxon:4577"

/tissue_type="tassel"

/dev_stage="just after the transition from vegetative to

inflorescence development"

/lab_host="XLOLR"

/clone_lib="946" - tassal primordium prepared by Schmidt

lab

/note="Organ: tassels; Vector: HybriZAP; Site:1: EcoRI;

Site_2: XhoI; George Chuck dissected immature tassels

between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

BASE COUNT 168 a 96 c 137 g 156 t

ORIGIN Query Match 41.5%; Score 550; DB 13; Length 557;
 Best local similarity 100.0%; Pred. No. 2.7e-47;
 Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 719 TCTTCTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAAAAAGAGAAAGGAAAAATTA 778

Db 1 TCTTCTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAAAAAGAGAAAGGAAAAATTA 60

Qy 779 TCAACATTGCATCTGATGTTGGTCTTACTGCGCAATGTTGCCAAGCTTAATATAGCGCAG 838

Db 61 TCAACATTGCATCTGATGTTGGTCTTACTGCGCAATGTTGCCAAGCTTAATATAGCGCAG 120

Qy 839 CCAAGGCTGGAGTGGTTTCACAAAACAGTTGCCAGGAGTATGCAAGCAAGAATA 898

Db 121 CCAAGGCTGGAGTGGTTTCACAAAACAGTTGCCAGGAGTATGCAAGCAAGAATA 180

Qy 899 TCAATGTGAATGCTATTGCACAGGGTTCAATTCATCTGATATCACTGCCCAACTTGGAG 958

Db 181 TCAATGTGAATGCTATTGCACAGGGTTCAATTCATCTGATATCACTGCCCAACTTGGAG 240

Qy 959 AGAGCTTGTAGAGAAATCTTGTCAACCAATTCGGTTAGGAGATATGCGCAACAGAGG 1018

Db 241 AGAGCTTGTAGAGAAATCTTGTCAACCAATTCGGTTAGGAGATATGCGCAACAGAGG 300

Qy 1019 AAGTTGCAGGGTTGGTCGAGTCTCTGGCCCTTAACCCGCGAGTATGACTGATGACTGGAC 1078

Db 301 AAGTTGCAGGGTTGGTCGAGTCTCTGGCCCTTAACCCGCGAGTATGACTGATGACTGGAC 360

Qy 1079 AGTGCTTACAAATTCGAGGAGGATGTAATGTAAGATTGTAGTTAGCTTGATGCACTTC 1138

Db 361 AGTGCTTACAAATTCGAGGAGGATGTAATGTAAGATTGTAGTTAGCTTGATGCACTTC 420

Qy 1139 TACTTTTGTGAGCAATTAATGTTGAACACCCCTTGTGTGTCACGGCGGATTTTGGACAAC 1198

Db 421 TACTTTTGTGAGCAATTAATGTTGAACACCCCTTGTGTGTCACGGCGGATTTTGGACAAC 480

Qy 1199 AATATGATGTTGCTCTCTCTTTTGTAACTCTCTGTAATAAATCTAGCATGTTGGAATG 1258

Db 481 AATATGATGTTGCTCTCTCTTTTGTAACTCTCTGTAATAAATCTAGCATGTTGGAATG 540

Qy 1259 GAAGTTGAAA 1268

Db 541 GAAGTTGAAA 550

RESULT 13

BM737475/c

LOCUS BM737475

DEFINITION 952056D06.y1.952 - BMS tissue from Walbot Lab (reduced rRNA) Zea

mays cDNA, mRNA sequence.

ACCESSION BM737475

VERSION BM737475.1 GI:19058808

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 589)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

JOURNAL

COMMENT

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 952056 row: D column: 06.

Location/Qualifiers

FEATURES

source

1. 589 /organism="Zea mays"
/mol_type="mRNA"
/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
/tissue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth phases"
/lab_host="DH10B"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

BASE COUNT 131 a 170 c 144 g 144 t

ORIGIN

Query Match 41.2%; Score 545.8; DB 12; Length 589;
Best Local Similarity 97.4%; Pred. No. 6.9e-47;
Matches 566; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

Qy 168 GCGGCCACCGCAGCAGCAGCAGTCTCTCCCGCGCTCGGTGGAGCAGCGGGGC 227
Db |

Qy 589 GCGCGCCACCGCAGCAGCAGTCTCTCCCGCGCTCGGTGGAGCAGCGGGGC 533
Db |

Qy 228 GCGCGCCCTCCCGCGGGGTTCGTACGTTGGTGGAGCGCGCGCTCTCTCC 287
Db |

Qy 532 GCGCGCCCTCCCGCGGGGTTCGTACGTTGGTGGAGCGCGCGCTCTCTCC 473
Db |

Qy 288 CACGCTGGGTCGCGCGGTGGTCTCTGGTGGCAACCCATGTTGCTGTGAACA 347
Db |

Qy 472 CACGCTGGGTCGCGCGGTGGTCTCTGGTGGCAACCCATGTTGCTGTGAACA 413
Db |

Qy 348 AGCAGTTGTAAGAATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTACAGGTGCATC 407
Db |

Qy 412 AGCAATTGTAAGAATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTACAGGTGCATC 353
Db |

Qy 408 TAGAGGATGGTAAGCAATGCTCTAGCCCTTGGAAAGCAGGATCAAGTTCTGGT 467
Db |

Qy 352 TAGAGGATGGTAAGCAATGCTCTAGCCCTTGGAAAGCAGGATCAAGTTCTGGT 293
Db |

Qy 468 AAATATGCGCGTCTCTGAAAGAGCTCAAGAGCTTCCAAAGAGATTGAAGCATCTGG 527
Db |

Qy 292 AAATATGCGCGTCTCTGAAAGAGCTTGAAGAGCTTCCAAAGAGATTGAAGCATCTGG 233
Db |

Qy 528 TGGTGAAGCATCACTTCGAGGAGATGTTTCAAAAGAGCTGATGATGATGATGAT 587
Db |

Qy 232 TGGTGAAGCATCACTTCGAGGAGATGTTTCAAAAGAGCTGATGATGATGATGAT 173
Db |

Qy 588 GAAAGCAGCTCTAGATAATGGGAACAATAGATGCTGTTAAATAGCGGATAC 647
Db |

Qy 172 GAAAGCAGCTCTAGATAATGGGAACAATAGATGCTGTTAAATAGCGGATAC 113
Db |

Qy 648 AGGACACATTTGATGAGATCAAGAAATCTCAGTGGCAGACGTAATGATCTGAA 707
Db |

Qy 112 AGGACACATTTGATGAGATCAAGAAATCTCAGTGGCAGACGTAATGATCTGAA 53
Db |

Qy 708 TCTTACTGCGCTCTCTTTGATGAGATCAAGAAATCTCAGTGGCAGACGTAATGATCTGAA 748
Db |

Qy 52 TCTTACTGCGCTCTCTTTGATGAGATCAAGAAATCTCAGTGGCAGACGTAATGATCTGAA 12
Db |

RESULT 14

CA830470

LOCUS

DEFINITION

CA830470 577 bp mRNA linear EST 12-DEC-2002

1117007C04.y1 1117 - Unigene V from Maize Genome Project Zea mays

cDNA, mRNA sequence.

ACCESSION

CA830470

VERSION

CA830470.1

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Zea mays

REFERENCE

Walbot, V.

AUTHORS

TITLE

Unpublished

JOURNAL

COMMENT

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1117007 row: C column: 04.

Location/Qualifiers

1. 577

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="taxon:4577"

/note="This library represents the unique genes found in the fifth round of EST sequencing at Stanford University for the maize genome project. Sequences are present from library 946. Contigs were assembled using ZMDAssembler and 2 representatives from each contig were selected for the Unigene set. All singlets were also selected."

BASE COUNT 122 a 170 c 160 g 125 t

ORIGIN

Query Match 40.6%; Score 538.2; DB 14; Length 577;

Best Local Similarity 97.6%; Pred. No. 4.2e-46;

Matches 569; Conservative 0; Mismatches 8; Indels 6; Gaps 2;

Qy 74 TACTCCCGCTGCATCTCCAAAGCAGCAGTCTCCCGCTTCCCGCTCTCTCGGCT 133

Db |

Qy 134 CTTTCGGCTCCGACGCGCCCTCTATGGCCACCGCGCGCGCCACCGCAGCAGCAGCAG 193

Db |

Qy 61 CTTTCGGCTCCGACGCGCCCTCTATGGCCACCGCGCGCGCCACCGCAGCAGCAGCAG 117

Db |

Qy 194 TCTCTCCCGCTGCAGTCCGAGCAGCAGCGCGCGCGCGCGCTCCCGCGCGGCTTCG 253

Db |

Qy 118 TCCTCTCCCGCTGCAGTCCGAGCAGCAGCGCGCGCGCGCTCCCGCGCGGCTTCG 174

Db |

Qy 254 TCAGTTTGGTGGAGGCGCGCGCTTCTCTCCACGCTGCGGTCCGCGCGGCTTCT 313

Db |

Qy 175 TCAGTTTGGTGGAGGCGCGCGCTTCTCTCCACGCTGCGGTCCGCGCGGCTTCT 234

Db |

Qy 314 CTGTTGTGCAACCCATGTTGCTGCTTTGAACAGCAGTTGTAAGATGCTACCAAGC 373

Db |

Qy 235 CTGTTGTGCAACCCATGTTGCTGCTTTGAACAGCAGTTGTAAGATGCTACCAAGC 294

Db |

Qy 374 TGGAGCTCCAGTTGTTGTTACAGTGCATCTAGAGGATGTTGAAGCACTGCTC 433

Db |

Qy 295 TGGAGCTCCAGTTGTTGTTGTTACAGTGCATCTAGAGGATGTTGAAGCACTGCTC 354

Db |

Qy 434 TAGCCCTTGAAGAGCAGGATGCAAGTTCTGTTAAATATGCGCGCTCTCCGAAAGG 493

Db |

Qy 355 TAGCCCTTGAAGAGCAGGATGCAAGTTCTGTTAAATATGCGCGCTCTCCGAAAGG 414

Db |

122	Db	TATCAACATTGCATCTGTAGTTGGTCTTACTGGCAATGTTGGCCCAAGCTAATTATAGCGC	181
837	Qy	AGCCAAGCTGGAGTGAATTCGGTTTCAAAAAACAGTTGCCAGGAGGATGCAAGCAGAAA	896
182	Db	AGCCNAGCTGGAGTGAATTCGGTTTCAAAAAACAGTTGCCAGGAGGATGCAAGCAGAAA	241
897	Qy	TATCAATGCTGAATCTGCTATTCGCACAGGGTTCATTGCATCTGATATAGCTACCGCAACTTGG	956
242	Db	TATCAATGCTGAATCTGCTATTCGCACAGGGTTCATTGCATCTGATATAGCTACCGCAACTTGG	301
957	Qy	AGAAAGCTTTGAGAAGAAAAATCTTGTCAACCAATTCCTTTAGGGGAGATATGGCCAAACCGA	1016
302	Db	AGAAAGCTTTGAGAAGAAAAATCTTGTCAACCAATTCCTTTAGGGGAGATATGGCCAAACCGA	361
1017	Qy	GGAAGTTGCAGGGTTGTCAGATCTCTGGCGCCTTAAACCCGCGACCTAGCTATATGACTGG	1076
362	Db	GGAAGTTGCAGGGTTGTCAGATCTCTGGCGCCTTAAACCCGCGACCTAGCTATATGACTGG	421
1077	Qy	ACAGTGCTTACAATTGACCGAGGGAATGTAATTAAGATTTGAGTTAGCTTGTATGCACT	1136
422	Db	ACAGTGCTTACAATTGACCGAGGGAATGTAATTAAGATTTGAGTTAGCTTGTATGCACT	481
1137	Qy	TCTACTTTTGTGTCAGCATTTTAATGTTGAAACACCCCTGTTGTGTCACGGCGGATTTTGGGA	1194
482	Db	TCTACTTTTGTGTCAGCATTTTAATGTTGAAACACCCCTGTTGTGTCACGGCGGATTTTGGGA	539

Search completed: November 7, 2003, 15:40:41
Job time : 3093 secs

Qy	494	CTGAAGAGGCTCTCAAAGAGATTGAAGCATCTGGTGTGAGGGCTATCACCTTCGGAGGAG	553
Db	415	CTGAAGAGGCTCTCAAAGAGATTGAAGCATCTGGTGTGAGGGCTATCACCTTCGGAGGAG	474
Qy	554	ATGTTTCAAAGAAGCTGATGTAGACTCTATGATGAAGCAGCTCTAGATAAATGGGAA	613
Db	475	ATGTTTCAAAGAAGCTGATGTAGACTCTATGATGAAGCAGCTCTAGATAAATGGGAA	534
Qy	614	CAATAGATGCTCTGGTAAATAATCAGGGATTACACGAGACAC	656
Db	535	CAATAGATGCTCTGGTAAATAATCAGGGATTACACGAGACAC	577

RESULT 15	
BU092794	539 bp mRNA linear EST 29-AUG-2002
LOCUS	946157G10.y1 946 - tassal primordium prepared by Schmidt lab Zea
DEFINITION	mays cDNA, mRNA sequence.
ACCESSION	BU092794
VERSION	BU092794.1 GI:22542341
KEYWORDS	EST.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 539)
TITLE	Walbot,V.V.
JOURNAL	Maize ESTs from various cDNA libraries sequenced at Stanford University
COMMENT	Unpublished Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 946157 row: G column: 10.

	Query Match	40.3%	Score 533.8;	DB 13;	Length 539;
	Best Local Similarity	99.4%;	Prod. No. 1.2e-45;		
	Matches 538;	Conservative	0; Mismatches 3;	Indels 0;	Gaps 0
QY	657	ATTGTTGATCAGGATCAGGAAGAAATCTCAGTGGCAAGACGTAATATGATCTCAATCTTACTTCGG	716		
DB	2	ACTGTTGATCAGGATGAAGAAATCTCAGTGGCAAGACGTAATATGATCTCAATCTTACTTCGG	61		
QY	717	CGTCTTCCTTTGTACACAGCGCTGCACAAAGTAAGTAATGATGAAAAGAGAAAGGGAATAAT	776		
DB	62	TGTCCTTCCTTTGTACACAGCGCTGCACAAAGTAATGATGAAAAGAGAAAGGGAATAAT	121		
QY	777	TATCAACATTGCATCTCTGATGTTGGTCTTATCTGGCAATGTTGGCCACAGCTTAATTATATACGC	836		

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 15:42:35 ; Search time 5006 Seconds
(without alignments)
10836.230 Million cell updates/sec

Title: US-10-024-806-1
Perfect score: 1326
Sequence: 1 gcygagcttccaaagccc.....aaaaaaaaaaaaaaaaaaaaa 1326

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_rod.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	50	3.8	3375	6	AR204971 Sequence
2	48	3.6	677	9	AB065088 Homo sapi
3	48	3.6	1210	3	AY069529 Drosophila
4	48	3.6	1522	6	AR153819 Sequence
5	48	3.6	2227	6	AR243792 Sequence
6	48	3.6	2877	9	BC018933 Homo sapi
7	48	3.6	2369	10	BC023786 Sequence
8	47	3.5	112	6	AX203306 Sequence
9	47	3.5	575	5	X65154 P.sativum G
10	47	3.5	679	8	AF467914 Danio rer
11	47	3.5	688	6	IO3321 Sequence 12
12	47	3.5	899	9	BC053374 Homo sapi
13	47	3.5	902	6	AX478009 Sequence
14	47	3.5	956	9	AL079309 Homo sapi
15	47	3.5	981	9	BC027909 Homo sapi
16	47	3.5	1015	6	BD082470 87 human
17	47	3.5	1100	17	AF111845 Homo sapi
18	47	3.5	1199	9	BC012540 Homo sapi
19	47	3.5	1201	6	AR243066 Sequence
20	47	3.5	1228	9	AL512750 Homo sapi
21	47	3.5	1265	3	AY119559 Drosophila
22	47	3.5	1275	8	AF297044 Zea mays
23	47	3.5	1358	9	BC013728 Homo sapi
24	47	3.5	1360	9	BC015168 Homo sapi
25	47	3.5	1400	8	AF239828 Petroseli
26	47	3.5	1552	9	BC002411 Homo sapi
27	47	3.5	1705	9	BC043560 Homo sapi
28	47	3.5	1750	9	BC048294 Homo sapi
29	47	3.5	1781	10	BC053434 Mus muscu
30	47	3.5	1911	10	BC048954 Mus muscu
31	47	3.5	2012	9	BC025740 Homo sapi
32	47	3.5	2059	3	AY069067 Drosophila
33	47	3.5	2100	3	BT001318 Drosophila
34	47	3.5	2150	9	BC012148 Homo sapi
35	47	3.5	2210	9	AB066547 Macaca fa
36	47	3.5	2332	9	BC007680 Homo sapi
37	47	3.5	2625	9	BC028978 Homo sapi
38	47	3.5	2651	9	BC013590 Homo sapi
39	47	3.5	2812	10	BC024323 Mus muscu
40	47	3.5	3340	9	BC038451 Homo sapi
41	47	3.5	3468	10	BC027246 Mus muscu
42	47	3.5	3706	3	AY069828 Drosophila
43	47	3.5	3965	9	BC034970 Homo sapi
44	47	3.5	3994	8	MB3471 N.plumbagin
45	47	3.5	4951	3	AY160092 Dictyoste
46	47	3.5	6548	5	BC047246 Xenopus l
47	47	3.5	64814	2	NCB21J21 Neurospor
48	47	3.5	152841	2	AL929463 Danio rer
49	47	3.5	183589	2	AC101777 Mus muscu
50	47	3.5	208409	2	AC117895 Rattus no
51	47	3.5	240901	2	AC096328 Rattus no
52	47	3.5	246548	2	BX530062 Danio rer
53	47	3.5	254050	3	PPA929358 Plasmodiu
54	46	3.5	130	6	BD116948 EST and e
55	46	3.5	227	9	BC046515 Homo sapi
56	46	3.5	255	3	AF132976 Buthus ma
57	46	3.5	255	6	BD113462 EST and e
58	46	3.5	347	6	A23327 O.sativa mR
59	46	3.5	347	6	I47730 Sequence 2
60	46	3.5	351	6	BD119190 EST and e
61	46	3.5	477	3	AF098065 Trypanoso
62	46	3.5	522	10	MUSKISTAE Li0730 Mouse (clon
63	46	3.5	529	5	BC045069 Xenopus l
64	46	3.5	530	6	AR243058 Sequence
65	46	3.5	532	8	AF001396 Oryza sat

Pred. No. is the number of results predicted by chance to have a

C	66	46	3.5	567	6	AX052527	AX052527 Sequence	139	46	3.5	1411	10	BC039806	BC039806 Mus muscu
	67	46	3.5	580	9	BC042082	BC042082 Homo sapi	140	46	3.5	1420	17	AF119899	AF119899 Homo sapi
	68	46	3.5	585	10	BC021916	BC021916 Mus muscu	141	46	3.5	1433	3	AB080950	AB080950 Ciona int
	69	46	3.5	589	10	BC002135	BC002135 Mus muscu	142	46	3.5	1437	3	BC032310	BC032310 Homo sapi
	70	46	3.5	610	8	AF009959	AF009959 Oryza sat	143	46	3.5	1451	17	AF118083	AF118083 Homo sapi
	71	46	3.5	615	3	AY075437	AY075437 Drosophi	144	46	3.5	1485	10	BC051057	BC051057 Mus muscu
	72	46	3.5	648	3	AY071113	AY071113 Drosophi	145	46	3.5	1493	9	BC042547	BC042547 Homo sapi
	73	46	3.5	659	3	AY119605	AY119605 Drosophi	146	46	3.5	1493	9	BC043317	BC043317 Homo sapi
	74	46	3.5	680	10	BC038677	BC038677 Mus muscu	147	46	3.5	1498	3	AY069685	AY069685 Drosophi
	75	46	3.5	691	3	HVU48513	U48594 Helicthis v	148	46	3.5	1499	5	BC045520	BC045520 Dario rer
	76	46	3.5	692	5	BC049029	BC049029 Dario rer	149	46	3.5	1499	5	BC032345	BC032345 Homo sapi
	77	46	3.5	699	9	AY080839	AY080839 Homo sapi	150	46	3.5	1502	10	BC023687	BC023687 Mus muscu
	78	46	3.5	703	9	AY080839	AY080839 Homo sapi	151	46	3.5	1503	5	BC041249	BC041249 Xenopus l
	79	46	3.5	728	3	AY069234	AY069234 Drosophi	152	46	3.5	1509	9	BC029059	BC029059 Homo sapi
	80	46	3.5	767	9	AK000653	AK000653 Homo sapi	153	46	3.5	1523	9	BC038956	BC038956 Homo sapi
	81	46	3.5	773	6	BD072968	BD072968 70 human	154	46	3.5	1540	9	BC035562	BC035562 Homo sapi
	82	46	3.5	775	9	BC027847	BC027847 Homo sapi	155	46	3.5	1541	9	HSN803748	AL832440 Homo sapi
	83	46	3.5	778	9	BC047942	BC047942 Homo sapi	156	46	3.5	1553	9	BC040262	BC040262 Homo sapi
	84	46	3.5	788	9	BC044829	BC044829 Homo sapi	157	46	3.5	1566	10	BC045149	BC045149 Mus muscu
	85	46	3.5	790	10	BC051504	BC051504 Mus muscu	158	46	3.5	1574	9	BC036048	BC036048 Homo sapi
	86	46	3.5	834	10	BC028766	BC028766 Mus muscu	159	46	3.5	1579	9	BC040355	BC040355 Homo sapi
	87	46	3.5	878	9	BC007499	BC007499 Homo sapi	160	46	3.5	1580	9	AK027109	AK027109 Homo sapi
	88	46	3.5	898	10	BC026633	BC026633 Mus muscu	161	46	3.5	1580	9	BC038840	BC038840 Homo sapi
	89	46	3.5	899	3	AK114040	AK114040 Ciona int	162	46	3.5	1596	8	PSVICK	X67429 Pisum sativ
	90	46	3.5	900	3	SIDERHYDA	Z21500 S. longipes	163	46	3.5	1615	9	AB050410	AB050410 Macaca fa
	91	46	3.5	901	6	AX305939	AX305939 Sequence	164	46	3.5	1617	10	BC024572	BC024572 Mus muscu
	92	46	3.5	901	10	MUSNASHY2	M68899 Mouse mast	165	46	3.5	1620	3	AY069829	AY069829 Drosophi
	93	46	3.5	923	3	AY070496	AY070496 Drosophi	166	46	3.5	1620	10	BC003888	BC003888 Mus muscu
	94	46	3.5	929	3	AY118282	AY118282 Drosophi	167	46	3.5	1626	9	AB060876	AB060876 Macaca fa
	95	46	3.5	930	3	AY075318	AY075318 Drosophi	168	46	3.5	1630	9	BC048341	BC048341 Homo sapi
	96	46	3.5	979	9	BC023583	BC023583 Homo sapi	169	46	3.5	1637	3	AK112340	AK112340 Ciona int
	97	46	3.5	985	9	BC051265	BC051265 Homo sapi	170	46	3.5	1637	6	AX460089	AX460089 Sequence
	98	46	3.5	1010	9	BC035795	BC035795 Homo sapi	171	46	3.5	1640	10	BC052156	BC052156 Mus muscu
	99	46	3.5	1020	3	AY118958	AY118958 Drosophi	172	46	3.5	1645	10	BC046317	BC046317 Mus muscu
	100	46	3.5	1020	8	AF236374	AF236374 Zea mays	173	46	3.5	1647	8	AF124842	AF124842 Capsicum
	101	46	3.5	1024	9	BC012602	BC012602 Homo sapi	174	46	3.5	1650	10	BC009332	BC009332 Homo sapi
	102	46	3.5	1027	9	BC035292	BC035292 Homo sapi	175	46	3.5	1653	10	BC018365	BC018365 Mus muscu
	103	46	3.5	1056	10	BC034844	BC034844 Mus muscu	176	46	3.5	1655	10	BC051403	BC051403 Mus muscu
	104	46	3.5	1057	5	BC047199	BC047199 Dario rer	177	46	3.5	1658	10	BC031470	BC031470 Mus muscu
	105	46	3.5	1065	6	AX644278	AX644278 Sequence	178	46	3.5	1660	6	AR243159	AR243159 Sequence
	106	46	3.5	1079	10	BC051970	BC051970 Mus muscu	179	46	3.5	1660	10	BC052328	BC052328 Mus muscu
	107	46	3.5	1084	9	BC009977	BC009977 Homo sapi	180	46	3.5	1662	9	BC011515	BC011515 Homo sapi
	108	46	3.5	1090	9	BC047013	BC047013 Homo sapi	181	46	3.5	1665	5	AF080068	AF080068 Xenopus l
	109	46	3.5	1097	10	BC008270	BC008270 Mus muscu	182	46	3.5	1686	9	BC025279	BC025279 Homo sapi
	110	46	3.5	1114	3	AY118558	AY118558 Drosophi	183	46	3.5	1688	9	AK025117	AK025117 Homo sapi
	111	46	3.5	1121	9	BC003658	BC003658 Homo sapi	184	46	3.5	1688	9	BC004899	BC004899 Homo sapi
	112	46	3.5	1126	10	BC022681	BC022681 Mus muscu	185	46	3.5	1690	9	BC037960	BC037960 Homo sapi
	113	46	3.5	1130	9	BC007659	BC007659 Homo sapi	186	46	3.5	1710	9	BC033591	BC033591 Homo sapi
	114	46	3.5	1144	10	BC028796	BC028796 Mus muscu	187	46	3.5	1736	9	BC016023	BC016023 Homo sapi
	115	46	3.5	1162	9	BC017328	BC017328 Homo sapi	188	46	3.5	1738	9	BC014399	BC014399 Homo sapi
	116	46	3.5	1168	9	BC042156	BC042156 Homo sapi	189	46	3.5	1743	10	BC051150	BC051150 Mus muscu
	117	46	3.5	1179	9	BC040374	BC040374 Homo sapi	190	46	3.5	1744	3	AY069796	AY069796 Drosophi
	118	46	3.5	1188	10	BC003972	BC003972 Mus muscu	191	46	3.5	1756	6	BD006863	BD006863 Drosophi
	119	46	3.5	1188	9	BC017237	BC017237 Homo sapi	192	46	3.5	1756	9	AF143723	AF143723 Homo sapi
	120	46	3.5	1200	10	BC030371	BC030371 Mus muscu	193	46	3.5	1758	9	BC018214	BC018214 Homo sapi
	121	46	3.5	1204	8	CAE275305	AJ275305 Cicer ari	194	46	3.5	1760	9	BC033862	BC033862 Homo sapi
	122	46	3.5	1207	9	BC024650	BC024650 Homo sapi	195	46	3.5	1761	9	BC006103	BC006103 Homo sapi
	123	46	3.5	1240	9	AK026633	AK026633 Homo sapi	196	46	3.5	1773	9	BC035667	BC035667 Homo sapi
	124	46	3.5	1240	10	BC030163	BC030163 Mus muscu	197	46	3.5	1776	9	HSN804574	HSN804574 Homo sapi
	125	46	3.5	1243	9	BC047691	BC047691 Homo sapi	198	46	3.5	1779	10	BC016197	BC016197 Mus muscu
	126	46	3.5	1257	9	AK027099	AK027099 Homo sapi	199	46	3.5	1780	9	BC020590	BC020590 Homo sapi
	127	46	3.5	1265	9	BC033301	BC033301 Homo sapi	200	46	3.5	1794	3	AB031232	AB031232 Toxoplas
	128	46	3.5	1273	9	BC020566	BC020566 Homo sapi	201	46	3.5	1796	9	AB070144	AB070144 Macaca fa
	129	46	3.5	1279	8	LSB297917	AJ297917 Lycopersi	202	46	3.5	1796	10	BC026588	BC026588 Mus muscu
	130	46	3.5	1307	10	BC038008	BC038008 Mus muscu	203	46	3.5	1796	10	BC026588	BC026588 Mus muscu
	131	46	3.5	1309	5	BC052141	BC052141 Dario rer	204	46	3.5	1798	8	AF521906	AF521906 Hebelona
	132	46	3.5	1330	9	BC037584	BC037584 Homo sapi	205	46	3.5	1802	9	AB047947	AB047947 Macaca fa
	133	46	3.5	1331	9	AK024588	AK024588 Homo sapi	206	46	3.5	1814	9	BC044249	BC044249 Homo sapi
	134	46	3.5	1357	10	BC026868	BC026868 Mus muscu	207	46	3.5	1816	9	BC041173	BC041173 Homo sapi
	135	46	3.5	1366	10	BC024950	BC024950 Mus muscu	208	46	3.5	1820	6	BD130976	BD130976 67 Human
	136	46	3.5	1368	10	BC020029	BC020029 Mus muscu	209	46	3.5	1832	9	BC025310	BC025310 Homo sapi
	137	46	3.5	1371	3	AY089518	AY089518 Drosophi	210	46	3.5	1841	9	AB072773	AB072773 Macaca fa
	138	46	3.5	1394	9	AK000418	AK000418 Homo sapi	211	46	3.5	1844	6	E16086	E16086 cDNA encodi
											1872	6	AR205050	AR205050 Sequence

212	46	3.5	1872	6	AX615066	Sequence	285	46	3.5	2530	9	BC037544	BC037544 Homo sapi
213	46	3.5	1878	9	HSMB03563	AL832256 Homo sapi	286	46	3.5	2532	9	HSMB05209	AL833903 Homo sapi
214	46	3.5	1890	9	BC050462	BC050462 Homo sapi	287	46	3.5	2538	9	BC014055	BC014055 Homo sapi
215	46	3.5	1900	3	AY113313	Drosophila	288	46	3.5	2540	9	BC053655	BC053655 Homo sapi
216	46	3.5	1902	9	AB047930	Macaca fa	289	46	3.5	2540	10	AB047324	AB047324 Rattus no
217	46	3.5	1902	9	BC048252	Homo sapi	290	46	3.5	2544	9	BC012343	BC012343 Homo sapi
218	46	3.5	1910	10	BC003738	Mus muscu	291	46	3.5	2560	9	AK027260	AK027260 Homo sapi
219	46	3.5	1913	9	BC017207	Homo sapi	292	46	3.5	2560	9	AB059653	AB059653 Macaca fa
220	46	3.5	1914	10	BC013523	Mus muscu	293	46	3.5	2604	9	HSMB05664	AL834537 Homo sapi
221	46	3.5	1927	5	BC045519	Danio rer	294	46	3.5	2605	9	BC036855	BC036855 Homo sapi
222	46	3.5	1935	10	BC026141	Mus muscu	295	46	3.5	2611	9	AK027152	AK027152 Homo sapi
223	46	3.5	1934	9	BC036327	Homo sapi	296	46	3.5	2619	9	AF068329	AF068329 Homo sapi
224	46	3.5	1965	3	AY069659	Drosophila	297	46	3.5	2625	6	AR164818	AR164818 Sequence
225	46	3.5	1968	10	BC027123	Mus muscu	298	46	3.5	2642	10	AS086166	AB086166 Mus muscu
226	46	3.5	1978	9	AK026762	Homo sapi	299	46	3.5	2666	3	AY069037	AY069037 Drosophila
227	46	3.5	1978	9	BC012750	Homo sapi	300	46	3.5	2674	5	BC051620	BC051620 Danio rer
228	46	3.5	1999	4	BTU52688	Bos taurus	301	46	3.5	2676	10	BC031754	BC031754 Mus muscu
229	46	3.5	2001	5	BC051623	Homo sapi	302	46	3.5	2690	10	BC051054	BC051054 Mus muscu
230	46	3.5	2026	9	BC022399	Homo sapi	303	46	3.5	2705	10	BC021341	BC021341 Mus muscu
231	46	3.5	2033	3	AK116646	Ciona int	304	46	3.5	2729	9	HSMB02938	X78627 H. sapiens m
232	46	3.5	2038	9	BC016758	Homo sapi	305	46	3.5	2758	9	HSMB02938	AL583915 Homo sapi
233	46	3.5	2038	9	BC043591	Homo sapi	306	46	3.5	2762	8	AFS30051	AFS30051 Chlamydom
234	46	3.5	2038	10	BC025004	Mus muscu	307	46	3.5	2783	9	BC027877	BC027877 Homo sapi
235	46	3.5	2043	10	BC052188	Mus muscu	308	46	3.5	2785	9	HSMB04684	AL833371 Homo sapi
236	46	3.5	2045	9	IR2004595	AL389957 Homo sapi	309	46	3.5	2807	9	BC047540	BC047540 Homo sapi
237	46	3.5	2059	9	BC025708	Homo sapi	310	46	3.5	2815	9	BC014834	BC014834 Homo sapi
238	46	3.5	2068	9	AF103804	Homo sapi	311	46	3.5	2825	3	AY070545	AY070545 Drosophila
239	46	3.5	2080	9	BC008717	Homo sapi	312	46	3.5	2826	9	BC040919	BC040919 Homo sapi
240	46	3.5	2081	10	BC043712	Mus muscu	313	46	3.5	2832	9	HSMB03459	AL832152 Homo sapi
241	46	3.5	2096	9	BC033808	Homo sapi	314	46	3.5	2837	6	AR083283	AR083283 Sequence
242	46	3.5	2105	9	BC017272	Homo sapi	315	46	3.5	2837	6	AX099547	AX099547 Sequence
243	46	3.5	2105	10	BC047133	Mus muscu	316	46	3.5	2837	6	BD056699	BD056699 Secreted
244	46	3.5	2111	9	HSMB05194	AL833893 Homo sapi	317	46	3.5	2897	6	AR088747	AR088747 Sequence
245	46	3.5	2112	6	AX535011	Sequence	318	46	3.5	2897	6	AR270600	AR270600 Sequence
246	46	3.5	2116	9	BC034379	Homo sapi	319	46	3.5	2897	9	HSU66075	U66075 Human trans
247	46	3.5	2128	10	BC049994	Mus muscu	320	46	3.5	2905	10	AY029302	AY029302 Rattus no
248	46	3.5	2130	3	AK112217	Ciona int	321	46	3.5	2955	10	BC025427	BC025427 Mus muscu
249	46	3.5	2130	9	BC032389	Homo sapi	322	46	3.5	2964	9	BC018366	BC018366 Homo sapi
250	46	3.5	2136	6	AX252575	Sequence	323	46	3.5	2967	9	BC044952	BC044952 Homo sapi
251	46	3.5	2136	6	AX376160	Sequence	324	46	3.5	2997	10	BC026819	BC026819 Mus muscu
252	46	3.5	2136	6	AX043415	Sequence	325	46	3.5	2997	10	MMPTA13A	X69026 M. musculus
253	46	3.5	2139	9	AY089322	Drosophila	326	46	3.5	3003	6	AX086957	AX086957 Sequence
254	46	3.5	2153	9	AB049880	Macaca fa	327	46	3.5	3003	9	HSMB01863	AL136895 Homo sapi
255	46	3.5	2159	9	HSMB00763	AL080234 Homo sapi	328	46	3.5	3006	6	AX497163	AX497163 Sequence
256	46	3.5	2177	9	BC043383	Homo sapi	329	46	3.5	3007	9	BC036087	BC036087 Homo sapi
257	46	3.5	2178	9	BC034740	Homo sapi	330	46	3.5	3040	9	BC036235	BC036235 Homo sapi
258	46	3.5	2209	9	BC034762	Homo sapi	331	46	3.5	3059	10	BC051082	BC051082 Mus muscu
259	46	3.5	2235	6	AR275257	Sequence	332	46	3.5	3072	10	BC026138	BC026138 Mus muscu
260	46	3.5	2235	6	AX049445	Sequence	333	46	3.5	3087	10	BC046972	BC046972 Mus muscu
261	46	3.5	2246	10	AF026124	Mus muscu	334	46	3.5	3122	9	BC030654	BC030654 Homo sapi
262	46	3.5	2256	3	AY069791	Drosophila	335	46	3.5	3122	9	BC041133	BC041133 Homo sapi
263	46	3.5	2267	6	E01314	cdna encodi	336	46	3.5	3169	5	AB031070	AB031070 Cyprinid
264	46	3.5	2283	9	AK000257	Homo sapi	337	46	3.5	3244	9	HSMB01107	AL117575 Homo sapi
265	46	3.5	2289	3	AK114795	Ciona int	338	46	3.5	3276	3	BT003295	BT003295 Drosophila
266	46	3.5	2296	9	HSMB02712	Homo sapi	339	46	3.5	3307	10	BC018613	BC018613 Mus muscu
267	46	3.5	2298	10	BC049257	Mus muscu	340	46	3.5	3347	9	HSMB03558	AL832251 Homo sapi
268	46	3.5	2322	9	BC028041	Homo sapi	341	46	3.5	3348	8	ATH011828	AT011628 Arabidops
269	46	3.5	2325	10	RNU30290	Rattus norv	342	46	3.5	3376	6	AX284970	AX284970 Sequence
270	46	3.5	2328	9	BC007567	Homo sapi	343	46	3.5	3386	9	HSMB00161	AL050092 Homo sapi
271	46	3.5	2345	9	AK027144	Homo sapi	344	46	3.5	3506	9	HSMB03163	AL831846 Homo sapi
272	46	3.5	2360	10	BC008547	Mus muscu	345	46	3.5	3513	6	AX277590	AX277590 Sequence
273	46	3.5	2389	9	BC014941	Homo sapi	346	46	3.5	3513	9	HSMB00944	AL117435 Homo sapi
274	46	3.5	2409	9	BC034925	Homo sapi	347	46	3.5	3521	6	AX382070	AX382070 Sequence
275	46	3.5	2437	9	BC018610	Homo sapi	348	46	3.5	3575	9	HSMB02410	AL137641 Homo sapi
276	46	3.5	2438	9	BC001056	Homo sapi	349	46	3.5	3587	10	BC016669	BC016669 Mus muscu
277	46	3.5	2438	9	BC001823	Homo sapi	350	46	3.5	3606	9	BC015897	BC015897 Homo sapi
278	46	3.5	2440	8	AB021862	Cucumis m	351	46	3.5	3619	9	HSMB05213	AL833907 Homo sapi
279	46	3.5	2445	9	BC048285	Homo sapi	352	46	3.5	3655	9	BC013382	BC013382 Homo sapi
280	46	3.5	2446	9	BC032448	Homo sapi	353	46	3.5	3710	9	BC035723	BC035723 Homo sapi
281	46	3.5	2462	9	HSMB00419	Homo sapi	354	46	3.5	3715	6	AR277694	AR277694 Sequence
282	46	3.5	2494	9	AF262032	Homo sapi	355	46	3.5	3715	10	MMU35846	U35846 Mus muscu
283	46	3.5	2514	9	BC049384	Homo sapi	356	46	3.5	3744	9	BC038299	BC038299 Homo sapi
284	46	3.5	2523	9	BC037218	Homo sapi	357	46	3.5	3838	9	BC026226	BC026226 Homo sapi

358	46	3.5	3860	9	BC035683	BC035683 Homo sapi	C 431	46	3.5	172132	9	AC010149	AC010149 Homo sapi
359	46	3.5	4010	9	BC035599	BC035599 Homo sapi	432	46	3.5	172665	10	AL645740	AL645740 Mouse DNA
360	46	3.5	4036	10	MWU278263	AJ278263 Mus muscu	433	46	3.5	176149	2	EX294129	EX294129 Danio rer
361	46	3.5	4080	10	BC051641	BC051641 Mus muscu	C 434	46	3.5	176149	2	EX294129	EX294129 Danio rer
362	46	3.5	4142	9	HSM800682	AL080163 Homo sapi	435	46	3.5	176440	9	AC0104675	AC0104675 Sus scrofa
363	46	3.5	4152	10	HSM803657	BC043657 Mus muscu	436	46	3.5	176601	9	AC073581	AC073581 Homo sapi
364	46	3.5	4212	9	HSM800772	AL110269 Homo sapi	437	46	3.5	177020	2	AC141484	AC141484 Mus muscu
365	46	3.5	4250	9	BC036749	BC036749 Homo sapi	438	46	3.5	177149	2	AC141484	AC141484 Mus muscu
366	46	3.5	4497	9	BC018928	BC018928 Homo sapi	439	46	3.5	178517	10	AC121905	AC121905 Mus muscu
367	46	3.5	4505	9	HSM803050	AL171378 Homo sapi	C 440	46	3.5	178981	10	AL806511	AL806511 Mouse DNA
368	46	3.5	4620	9	BC033494	BC033494 Homo sapi	C 441	46	3.5	179548	2	AC131596	AC131596 Mus muscu
369	46	3.5	4656	9	HSM803142	AL831828 Homo sapi	442	46	3.5	180849	2	AC131596	AC131596 Mus muscu
370	46	3.5	4730	9	BC036755	AL831828 Homo sapi	443	46	3.5	181834	2	AC131596	AC131596 Mus muscu
371	46	3.5	4869	3	AY113238	AY113238 Drosophila	C 444	46	3.5	183412	2	AP001899	AP001899 Homo sapi
372	46	3.5	5120	6	AX710220	AX710220 Sequence	445	46	3.5	184121	9	AC016706	AC016706 Homo sapi
373	46	3.5	5130	9	HSM801717	AL136749 Homo sapi	C 446	46	3.5	186574	2	AC123827	AC123827 Mus muscu
374	46	3.5	5440	6	AX710219	AX710219 Sequence	C 447	46	3.5	187904	2	AC119843	AC119843 Mus muscu
375	46	3.5	5465	3	AY051653	AY051653 Drosophila	C 448	46	3.5	190517	9	CNS01DX4	AL139022 Human chr
376	46	3.5	5856	9	HSM803500	AL83193 Homo sapi	C 449	46	3.5	191733	10	AC121774	AC121774 Mus muscu
377	46	3.5	6153	6	BD160662	BD160662 Primer fo	450	46	3.5	193108	10	AL671977	AL671977 Mouse DNA
378	46	3.5	6153	9	AK027868	AK027868 Homo sapi	C 451	46	3.5	193108	10	AL671977	AL671977 Mouse DNA
379	46	3.5	6251	10	BC050823	BC050823 Mus muscu	452	46	3.5	196421	10	AL672100	AL672100 Mouse DNA
380	46	3.5	6410	9	AF230496	AF230496 Homo sapi	453	46	3.5	196469	2	EX465218	EX465218 Mus muscu
C 381	46	3.5	6660	10	AF447901S2	AF447902 Mus muscu	C 454	46	3.5	198185	2	AC131323	AC131323 Mus muscu
382	46	3.5	6791	6	AG0092	AG0092 Sequence 2	455	46	3.5	198341	10	AL122454	AC122454 Mus muscu
383	46	3.5	10195	6	AG0094	AG0094 Sequence 4	456	46	3.5	199394	10	AL732370	AL732370 Mouse DNA
384	46	3.5	10919	10	AF031572	AF031572 Mus muscu	C 457	46	3.5	199394	10	AL732370	AL732370 Mouse DNA
385	46	3.5	12029	3	AE001400	AE001400 Plasmodiu	458	46	3.5	200059	9	AL355136	AL355136 Human DNA
C 386	46	3.5	12463	3	AC115578	AC115578 Dictyoste	459	46	3.5	200075	2	AC127302	AC127302 Mus muscu
387	46	3.5	33651	3	AC114261	AC114261 Dictyoste	C 460	46	3.5	200616	2	AC132240	AC132240 Mus muscu
C 388	46	3.5	37599	9	AP000532	AP000532 Homo sapi	C 461	46	3.5	203422	10	AL713863	AL713863 Mouse DNA
389	46	3.5	38692	3	AC116919	AC116919 Dictyoste	C 462	46	3.5	204166	2	AC121451	AC121451 Rattus no
390	46	3.5	40992	9	AC002471	AC002471 Homo sapi	463	46	3.5	207823	2	AC114425	AC114425 Mus muscu
391	46	3.5	41958	5	AC005374	AC005374 Homo sapi	464	46	3.5	210005	2	AC118299	AC118299 Rattus no
C 392	46	3.5	80272	5	AL591180	AL591180 Zebrafish	465	46	3.5	212410	2	AC118804	AC118804 Rattus no
C 393	46	3.5	82848	5	AL645689	AL645689 Zebrafish	C 466	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 394	46	3.5	89232	5	AL591175	AL591175 Zebrafish	C 467	46	3.5	212838	2	AC134843	AC134843 Mus muscu
C 395	46	3.5	92496	5	AL589848	AL589848 Human DNA	C 468	46	3.5	213684	10	AC132616	AC132616 Mus muscu
C 396	46	3.5	109143	10	AL845448	AL845448 Mouse DNA	C 469	46	3.5	214508	2	AC103532	AC103532 Rattus no
C 397	46	3.5	110000	2	AC102983	Continuation (2 of	470	46	3.5	214792	2	AC118038	AC118038 Mus muscu
C 398	46	3.5	110000	2	AC111440	Continuation (2 of	471	46	3.5	216064	2	AC137117	AC137117 Mus muscu
C 399	46	3.5	110000	2	EX005003	Continuation (3 of	C 472	46	3.5	219111	10	EX284639	EX284639 Mus muscu
C 400	46	3.5	110000	2	EX284615	Continuation (3 of	C 473	46	3.5	219368	10	AC098721	AC098721 Mus muscu
C 401	46	3.5	110000	2	EX232863	Continuation (3 of	474	46	3.5	219752	2	AC115297	AC115297 Mus muscu
C 402	46	3.5	110000	3	AC116305	Continuation (4 of	475	46	3.5	220036	2	AC135494	AC135494 Rattus no
C 403	46	3.5	110000	3	AC116984	AC116984 Dictyoste	C 476	46	3.5	220218	9	AC006288	AC006288 Homo sapi
C 404	46	3.5	110000	3	AC116984	Continuation (4 of	C 477	46	3.5	221680	2	AC107045	AC107045 Mus muscu
C 405	46	3.5	123701	9	AC010137	AC010137 Homo sapi	C 478	46	3.5	225314	2	EX004798	EX004798 Mus muscu
C 406	46	3.5	135774	2	AC091380	AC091380 Mus muscu	C 479	46	3.5	225462	2	AL929345	AL929345 Danio rer
C 407	46	3.5	136956	2	AC137338	AC137338 Rattus no	C 480	46	3.5	226784	2	AL845476	AL845476 Mus muscu
C 408	46	3.5	137648	2	AC024316	AC024316 Homo sapi	C 481	46	3.5	228826	2	AC135589	AC135589 Rattus no
C 409	46	3.5	141009	2	AC009425	AC009425 Homo sapi	C 482	46	3.5	229084	2	AC096384	AC096384 Rattus no
C 410	46	3.5	142100	2	EX511181	EX511181 Danio rer	483	46	3.5	229724	10	AL669964	AL669964 Mouse DNA
C 411	46	3.5	14570	3	AC117072	AC117072 Dictyoste	C 484	46	3.5	230362	2	AC074225	AC074225 Mus muscu
C 412	46	3.5	147952	9	AC008712	AC008712 Homo sapi	C 485	46	3.5	231108	2	AC141480	AC141480 Mus muscu
C 413	46	3.5	148295	2	AL662913	AL662913 Homo sapi	C 486	46	3.5	231108	2	AC141480	AC141480 Mus muscu
C 414	46	3.5	150509	2	AC113453	AC113453 Mus muscu	C 487	46	3.5	231235	2	AC121595	AC121595 Mus muscu
C 415	46	3.5	152829	2	AC132267	AC132267 Mus muscu	C 488	46	3.5	231337	2	EX537289	EX537289 Danio rer
C 416	46	3.5	153139	2	AC129296	AC129296 Mus muscu	C 489	46	3.5	232634	2	AC099727	AC099727 Mus muscu
C 417	46	3.5	153228	2	AC139129	AC139129 Mus muscu	C 490	46	3.5	240154	2	AC094137	AC094137 Rattus no
C 418	46	3.5	153228	2	AC139129	AC139129 Mus muscu	C 491	46	3.5	240853	2	AC142057	AC142057 Rattus no
C 419	46	3.5	156446	2	AC144774	AC144774 Mus muscu	C 492	46	3.5	244974	2	AC097706	AC097706 Rattus no
C 420	46	3.5	157667	2	AC115970	AC115970 Mus muscu	C 493	46	3.5	245382	2	AC114187	AC114187 Rattus no
C 421	46	3.5	161674	10	AL807394	AL807394 Mouse DNA	494	46	3.5	245569	2	AC113818	AC113818 Rattus no
C 422	46	3.5	161931	2	AC117903	AC117903 Rattus no	C 495	46	3.5	247840	2	AC130394	AC130394 Rattus no
C 423	46	3.5	163829	2	AC136048	AC136048 Rattus no	C 496	46	3.5	248403	2	AC096264	AC096264 Rattus no
C 424	46	3.5	165104	2	EX511213	EX511213 Danio rer	C 497	46	3.5	250714	2	AC094792	AC094792 Rattus no
C 425	46	3.5	167357	2	AC023873	AC023873 Homo sapi	C 498	46	3.5	252966	2	AC108538	AC108538 Rattus no
C 426	46	3.5	167409	10	AC121982	AC121982 Mus muscu	C 499	46	3.5	268325	5	AL954838	AL954838 Zebrafish
C 427	46	3.5	168544	9	AL133344	AL133344 Human DNA	500	46	3.5	293405	2	AC096156	AC096156 Rattus no
C 428	46	3.5	169825	2	AC102577	AC102577 Mus muscu	C 501	46	3.5	302156	3	AC116977	AC116977 Dictyoste
C 429	46	3.5	170053	2	AC133069	AC133069 Macaca mu	C 502	46	3.5	319938	2	AC107444	AC107444 Rattus no
C 430	46	3.5	171076	2	AC101857	AC101857 Mus muscu	503	46	3.5	331039	3	AC116988	AC116988 Dictyoste

504	46	3.5	332036	2	AC129629	AC129629 Rattus no	577	45	3.4	958	6	AR217518	AR217518 Sequence
505	46	3.5	343753	2	AC129332	AC129332 Mus muscu	578	45	3.4	958	6	AR233975	AR233975 Sequence
506	46	3.5	346007	2	BD114921	BD114921 Mus muscu	579	45	3.4	958	6	AX250563	AX250563 Sequence
507	45	3.4	91	91	BD118981	BD118981 EST and e	580	45	3.4	958	6	BD056504	BD056504 Apparatus
508	45	3.4	184	6	BD116949	BD116949 EST and e	581	45	3.4	958	6	BD137222	BD137222 Luciferas
509	45	3.4	188	6	AX341368	AX341368 Sequence	582	45	3.4	958	6	E01573	E01573 cDNA sequen
510	45	3.4	293	6	AX187087	AX187087 Sequence	583	45	3.4	958	6	E01575	E01575 cDNA sequen
511	45	3.4	308	6	AX329898	AX329898 Sequence	584	45	3.4	958	6	E02319	E02319 DNA encodin
512	45	3.4	308	6	AX330637	AX330637 Sequence	585	45	3.4	980	9	HSM800632	HSM800632 Homo sapi
513	45	3.4	308	6	AX330821	AX330821 Sequence	586	45	3.4	985	9	HS4420492	HS4420492 Homo sapi
514	45	3.4	332	6	AX185622	AX185622 Sequence	587	45	3.4	992	9	HSRANAP1	HSRANAP1 H.sapiens m
515	45	3.4	358	6	BD108843	BD108843 EST and e	588	45	3.4	1022	8	AF179295	AF179295 Malus dom
516	45	3.4	372	9	BD015361	BD015361 Homo sapi	589	45	3.4	1026	9	AK027111	AK027111 Homo sapi
517	45	3.4	380	9	HSWUC5BR	Y1080 H.sapiens M	590	45	3.4	1028	10	BC002172	BC002172 Mus muscu
518	45	3.4	447	9	AK026855	AK026855 Homo sapi	591	45	3.4	1030	9	BC000895	BC000895 Homo sapi
519	45	3.4	473	9	BC051840	BC051840 Homo sapi	592	45	3.4	1032	8	AF043538	AF043538 Arabidops
520	45	3.4	476	8	AY157064	AY157064 Lycopersi	593	45	3.4	1035	3	CIN431687	CIN431687 Ciona int
521	45	3.4	488	9	BC003678	BC003678 Homo sapi	594	45	3.4	1040	9	BC036737	BC036737 Homo sapi
522	45	3.4	512	3	AK115390	AK115390 Ciona int	595	45	3.4	1042	9	BC021232	BC021232 Homo sapi
523	45	3.4	518	8	QSAJ692	AJ000692 Quercus s	596	45	3.4	1045	3	AY075210	AY075210 Drosophil
524	45	3.4	561	10	BC049674	BC049674 Mus muscu	597	45	3.4	1055	9	BC022357	BC022357 Homo sapi
525	45	3.4	570	3	AK112184	AK112184 Ciona int	598	45	3.4	1058	10	BC052508	BC052508 Mus muscu
526	45	3.4	574	9	AK025408	AK025408 Homo sapi	599	45	3.4	1075	6	AR150950	AR150950 Sequence
527	45	3.4	595	6	AX090442	AX090442 Sequence	600	45	3.4	1078	10	AF391160	AF391160 Mus muscu
528	45	3.4	602	9	BC008488	BC008488 Homo sapi	601	45	3.4	1081	3	AY069038	AY069038 Drosophil
529	45	3.4	631	10	BC049570	BC049570 Mus muscu	602	45	3.4	1088	3	BT003646	BT003646 Drosophil
530	45	3.4	691	6	AX011676	AX011676 Sequence	603	45	3.4	1091	6	AR271010	AR271010 Sequence
531	45	3.4	705	8	AF180373	AF180373 Medicago	604	45	3.4	1091	6	AX053122	AX053122 Sequence
532	45	3.4	726	3	AY094790	AY094790 Drosophil	605	45	3.4	1107	9	BC014072	BC014072 Homo sapi
533	45	3.4	740	6	AK066486	AK066486 Sequence	606	45	3.4	1110	9	BC033649	BC033649 Homo sapi
534	45	3.4	740	6	AR074039	AR074039 Sequence	607	45	3.4	1112	9	BC009201	BC009201 Homo sapi
535	45	3.4	740	6	AR143611	AR143611 Sequence	608	45	3.4	1116	9	BC039532	BC039532 Homo sapi
536	45	3.4	740	6	AR216334	AR216334 Sequence	609	45	3.4	1120	9	BC043377	BC043377 Homo sapi
537	45	3.4	740	6	BD005647	BD005647 Materials	610	45	3.4	1126	5	AB090368	AB090368 Takifugu
538	45	3.4	741	6	AR074149	AR074149 Sequence	611	45	3.4	1127	3	AK115583	AK115583 Ciona int
539	45	3.4	741	6	AR216384	AR216384 Sequence	612	45	3.4	1129	9	BC013587	BC013587 Homo sapi
540	45	3.4	741	6	BD005697	BD005697 Materials	613	45	3.4	1139	9	BC030517	BC030517 Homo sapi
541	45	3.4	745	9	BC047941	BC047941 Homo sapi	614	45	3.4	1141	10	BC023104	BC023104 Mus muscu
542	45	3.4	751	9	AF412816	AF412816 Homo sapi	615	45	3.4	1145	10	BC024912	BC024912 Mus muscu
543	45	3.4	752	9	AF475095	AF475095 Homo sapi	616	45	3.4	1152	9	BC021621	BC021621 Homo sapi
544	45	3.4	756	6	AX046859	AX046859 Sequence	617	45	3.4	1157	9	BC013427	BC013427 Homo sapi
545	45	3.4	764	9	AK047904	AK047904 Macaca fa	618	45	3.4	1159	17	AF119883	AF119883 Homo sapi
546	45	3.4	768	10	BC019779	BC019779 Mus muscu	619	45	3.4	1161	9	BC015991	BC015991 Homo sapi
547	45	3.4	781	10	BC028530	BC028530 Mus muscu	620	45	3.4	1182	10	BC003890	BC003890 Mus muscu
548	45	3.4	783	8	CCFCP10	AJ000972 Cyclostell	621	45	3.4	1189	9	AK026104	AK026104 Homo sapi
549	45	3.4	783	9	BC017733	BC017733 Homo sapi	622	45	3.4	1203	10	BC031854	BC031854 Mus muscu
550	45	3.4	788	6	AR216422	AR216422 Sequence	623	45	3.4	1212	6	AR210335	AR210335 Sequence
551	45	3.4	822	10	BC028504	BC028504 Mus muscu	624	45	3.4	1212	9	AF100781	AF100781 Homo sapi
552	45	3.4	826	6	E08516	E08516 DNA encodin	625	45	3.4	1212	9	AF100781	AF100781 Homo sapi
553	45	3.4	826	6	E12586	E12586 cDNA encodi	626	45	3.4	1228	9	BC002577	BC002577 Homo sapi
554	45	3.4	826	8	S65048	S65048 self-incomp	627	45	3.4	1229	10	BC030860	BC030860 Mus muscu
555	45	3.4	834	10	AF115410	AF115410 Cricetulu	628	45	3.4	1230	5	BC046022	BC046022 Danio rer
556	45	3.4	835	8	ATP27A	Y11792 A.thaliana	629	45	3.4	1243	9	BC034709	BC034709 Homo sapi
557	45	3.4	840	10	AX105299	AX105299 Sequence	630	45	3.4	1243	9	HSM802621	HSM802621 Homo sapi
558	45	3.4	844	6	AX105299	BC026668 Mus muscu	631	45	3.4	1256	17	AF119894	AF119894 Homo sapi
559	45	3.4	848	5	BC044005	BC044005 Xenopus l	632	45	3.4	1263	6	AX546767	AX546767 Sequence
560	45	3.4	848	10	BC018351	BC018351 Mus muscu	633	45	3.4	1271	10	AF161699	AF161699 Mus muscu
561	45	3.4	861	9	AK026600	AK026600 Homo sapi	634	45	3.4	1286	10	BC019521	BC019521 Mus muscu
562	45	3.4	874	10	BC043922	BC043922 Mus muscu	635	45	3.4	1289	10	BC026842	BC026842 Mus muscu
563	45	3.4	887	9	BC015166	BC015166 Homo sapi	636	45	3.4	1296	9	BC009221	BC009221 Homo sapi
564	45	3.4	920	9	BC041137	BC041137 Homo sapi	637	45	3.4	1299	10	BC021404	BC021404 Mus muscu
565	45	3.4	921	10	BC006040	BC006040 Mus muscu	638	45	3.4	1303	10	BC004060	BC004060 Mus muscu
566	45	3.4	925	3	AEVQA440X	L29571 Aequorea vi	639	45	3.4	1307	6	AX578117	AX578117 Sequence
567	45	3.4	932	9	BC047912	BC047912 Homo sapi	640	45	3.4	1313	9	AB048994	AB048994 Macaca fa
568	45	3.4	938	6	A70386	A70386 Sequence 16	641	45	3.4	1315	6	AR173812	AR173812 Sequence
569	45	3.4	938	6	BD010516	BD010516 A novel h	642	45	3.4	1315	10	AF082526	AF082526 Mus muscu
570	45	3.4	941	6	BD010547	BD010547 A novel h	643	45	3.4	1317	10	BC038528	BC038528 Mus muscu
571	45	3.4	941	6	A15345	A15345 Bam HI huma	644	45	3.4	1331	10	BC030915	BC030915 Mus muscu
572	45	3.4	941	6	I03096	I03096 Sequence 8	645	45	3.4	1340	6	AX704811	AX704811 Sequence
573	45	3.4	953	3	TVCP4	X77221 T.vaginalis	646	45	3.4	1346	9	BC042079	BC042079 Homo sapi
574	45	3.4	958	6	AR108851	AR108851 Sequence	647	45	3.4	1347	9	AK026504	AK026504 Homo sapi
575	45	3.4	958	6	AR119320	AR119320 Sequence	648	45	3.4	1351	9	BC004261	BC004261 Homo sapi
576	45	3.4	958	6	AR151721	AR151721 Sequence	649	45	3.4	1360	10	BC046762	BC046762 Mus muscu

650	45	3.4	1372	9	HSN800085	Al0493300 Homo sapi	723	45	3.4	1797	6	AX236928	Sequence
651	45	3.4	1373	10	BC049731	BC049731 Mus muscu	724	45	3.4	1799	9	BC030249	Homo sapi
652	45	3.4	1389	9	BC006210	BC006210 Homo sapi	725	45	3.4	1807	9	BC029917	Homo sapi
653	45	3.4	1400	10	BC037690	BC037690 Mus muscu	726	45	3.4	1817	9	BC051809	Homo sapi
654	45	3.4	1406	9	BC011912	BC011912 Homo sapi	727	45	3.4	1822	3	AY051627	Drosophil
655	45	3.4	1417	9	BC043372	BC043372 Homo sapi	728	45	3.4	1825	9	BC015110	Homo sapi
656	45	3.4	1417	9	BC028022	BC028022 Homo sapi	729	45	3.4	1827	5	BC049315	Danio rer
657	45	3.4	1427	9	BC028022	BC028022 Homo sapi	730	45	3.4	1827	5	BC034435	Homo sapi
658	45	3.4	1431	3	AK116801	AK116801 Clona int	731	45	3.4	1830	9	BC035749	Homo sapi
659	45	3.4	1435	10	BC015086	BC015086 Mus muscu	732	45	3.4	1833	9	BC041158	Homo sapi
660	45	3.4	1443	9	HSN802527	BC018470 Mus muscu	733	45	3.4	1835	6	AR202048	Sequence
661	45	3.4	1448	9	BC038355	BC038355 Homo sapi	734	45	3.4	1837	10	S69385	epithelial
662	45	3.4	1449	9	BC011460	BC011460 Homo sapi	735	45	3.4	1853	9	HSU58996	US9896 Homo sapien
663	45	3.4	1459	3	AK113466	AK113466 Clona int	736	45	3.4	1857	3	AY113330	Drosophil
664	45	3.4	1463	10	BC005424	BC005424 Mus muscu	737	45	3.4	1860	5	BC046076	Danio rer
665	45	3.4	1464	10	BC002075	BC002075 Mus muscu	738	45	3.4	1868	9	AK026549	Homo sapi
666	45	3.4	1464	10	BC008974	BC008974 Mus muscu	739	45	3.4	1870	9	AB048881	Macaca fa
667	45	3.4	1471	9	BC018762	BC018762 Homo sapi	740	45	3.4	1873	17	AF119859	AF119859 Homo sapi
668	45	3.4	1472	9	BC018762	BC018762 Homo sapi	741	45	3.4	1876	10	BC053422	Mus muscu
669	45	3.4	1481	10	BC049618	BC049618 Mus muscu	742	45	3.4	1879	9	HSN801116	AL117583 Homo sapi
670	45	3.4	1501	10	BC020094	BC020094 Mus muscu	743	45	3.4	1881	9	HSN801116	AL117583 Homo sapi
671	45	3.4	1511	10	BC026543	BC026543 Mus muscu	744	45	3.4	1886	9	AK025084	AY051798 Drosophil
672	45	3.4	1523	10	BC027442	BC027442 Mus muscu	745	45	3.4	1892	3	AY051798	AY051798 Drosophil
673	45	3.4	1523	17	AF116614	AF116614 Homo sapi	746	45	3.4	1906	9	AB071106	AB071106 Macaca fa
674	45	3.4	1528	9	BC042956	BC042956 Homo sapi	747	45	3.4	1909	10	BC040747	BC040747 Mus muscu
675	45	3.4	1534	9	BC008416	BC008416 Homo sapi	748	45	3.4	1913	10	BC003999	BC003999 Mus muscu
676	45	3.4	1539	10	BC053448	BC053448 Mus muscu	749	45	3.4	1938	9	BC043555	BC043555 Homo sapi
677	45	3.4	1541	3	AK115753	AK115753 Clona int	750	45	3.4	1946	5	BC053207	BC053207 Danio rer
678	45	3.4	1552	10	BC026370	BC026370 Mus muscu	751	45	3.4	1948	9	AK026687	AK026687 Homo sapi
679	45	3.4	1560	9	BC035572	BC035572 Homo sapi	752	45	3.4	1948	9	BC044241	Homo sapi
680	45	3.4	1573	3	LVU25082	LVU25082 Loliigo vu	753	45	3.4	1959	9	BC040005	Homo sapi
681	45	3.4	1580	9	BC035599	BC035599 Homo sapi	754	45	3.4	1977	9	AB056792	AB056792 Macaca fa
682	45	3.4	1583	9	BC029035	BC029035 Homo sapi	755	45	3.4	1981	3	AY070835	AY070835 Drosophil
683	45	3.4	1592	8	AF019630	AF019630 Magnaport	756	45	3.4	1985	8	AF157059	AF157059 Artemisia
684	45	3.4	1595	9	BC040734	BC040734 Homo sapi	757	45	3.4	1988	9	AB093636	AB093636 Macaca fa
685	45	3.4	1606	10	BC051117	BC051117 Mus muscu	758	45	3.4	2009	5	BC044124	BC044124 Xenopus l
686	45	3.4	1616	10	BC010327	BC010327 Mus muscu	759	45	3.4	2019	3	AY058686	AY058686 Drosophil
687	45	3.4	1628	3	AY118763	AY118763 Drosophil	760	45	3.4	2019	9	BC004920	BC004920 Homo sapi
688	45	3.4	1630	9	BC039130	BC039130 Homo sapi	761	45	3.4	2022	10	BC046446	BC046446 Mus muscu
689	45	3.4	1640	9	AB070034	AB070034 Macaca fa	762	45	3.4	2023	3	AY119490	AY119490 Drosophil
690	45	3.4	1642	10	BC014817	BC014817 Mus muscu	763	45	3.4	2031	10	MMPTROM	MMPTROM Mouse mRNA
691	45	3.4	1654	3	BRPCHIT	M73689 Brugia mala	764	45	3.4	2035	6	IO8608	IO8608 Sequence 3
692	45	3.4	1657	6	EL1332	EL1332 Human cDNA	765	45	3.4	2067	9	BC008732	BC008732 Homo sapi
693	45	3.4	1659	6	AX237691	AX237691 Sequence	766	45	3.4	2073	9	HSN801468	HSN801468 Homo sapi
694	45	3.4	1659	9	HUMP57B	D44497 Human mRNA	767	45	3.4	2080	10	BC013564	BC013564 Mus muscu
695	45	3.4	1661	10	AF081366	AF081366 Rattus no	768	45	3.4	2096	9	BC050272	BC050272 Homo sapi
696	45	3.4	1664	9	BC028227	BC028227 Homo sapi	769	45	3.4	2098	9	BC011820	BC011820 Homo sapi
697	45	3.4	1665	9	BC041446	BC041446 Homo sapi	770	45	3.4	2115	9	BC018318	BC018318 Homo sapi
698	45	3.4	1673	10	BC010324	BC010324 Mus muscu	771	45	3.4	2150	6	AX210648	AX210648 Sequence
699	45	3.4	1679	9	BC033143	BC033143 Homo sapi	772	45	3.4	2150	9	AF017790	AF017790 Homo sapi
700	45	3.4	1688	9	BC000115	BC000115 Homo sapi	773	45	3.4	2151	10	BC027381	BC027381 Mus muscu
701	45	3.4	1709	9	BC039890	BC039890 Homo sapi	774	45	3.4	2173	10	BC048927	BC048927 Mus muscu
702	45	3.4	1711	6	BD063242	BD063242 Secreted	775	45	3.4	2176	10	BC034399	BC034399 Mus muscu
703	45	3.4	1712	5	BC049516	BC049516 Danio rer	776	45	3.4	2180	9	BC035809	BC035809 Homo sapi
704	45	3.4	1724	9	BC002454	BC002454 Homo sapi	777	45	3.4	2187	10	BC046283	BC046283 Mus muscu
705	45	3.4	1728	6	AR117141	AR117141 Sequence	778	45	3.4	2198	9	HSN803382	HSN803382 Homo sapi
706	45	3.4	1728	6	AR254116	AR254116 Sequence	779	45	3.4	2227	9	BC004934	BC004934 Homo sapi
707	45	3.4	1728	6	BD023469	BD023469 Isolated	780	45	3.4	2229	9	BC050571	BC050571 Homo sapi
708	45	3.4	1728	9	AF013249	AF013249 Homo sapi	781	45	3.4	2229	9	HSN803552	HSN803552 Homo sapi
709	45	3.4	1729	9	BC039813	BC039813 Homo sapi	782	45	3.4	2240	4	AB042653	AB042653 Bos tauru
710	45	3.4	1732	3	AY118611	AY118611 Drosophil	783	45	3.4	2240	9	BC034937	BC034937 Homo sapi
711	45	3.4	1746	5	BC052142	BC052142 Danio rer	784	45	3.4	2245	9	BC028076	BC028076 Homo sapi
712	45	3.4	1763	9	BC041473	BC041473 Homo sapi	785	45	3.4	2246	9	BC051820	BC051820 Homo sapi
713	45	3.4	1764	3	AY069232	AY069232 Drosophil	786	45	3.4	2249	10	BC024533	BC024533 Mus muscu
714	45	3.4	1767	3	AY069170	AY069170 Drosophil	787	45	3.4	2255	3	AY089465	AY089465 Drosophil
715	45	3.4	1771	3	AK116800	AK116800 Clona int	788	45	3.4	2260	6	BD021751	BD021751 Novel gen
716	45	3.4	1773	9	BC037559	BC037559 Homo sapi	789	45	3.4	2260	6	BD083722	BD083722 Nucleic a
717	45	3.4	1776	5	BC045989	BC045989 Danio rer	790	45	3.4	2260	6	BD097369	BD097369 Nucleic a
718	45	3.4	1776	6	AR099768	AR099768 Sequence	791	45	3.4	2260	6	BD101689	BD101689 Novel gen
719	45	3.4	1776	6	AR202548	AR202548 Sequence	792	45	3.4	2293	9	BC043566	BC043566 Homo sapi
720	45	3.4	1776	8	NTU38446	NTU38446 Sequence	793	45	3.4	2296	9	BC013573	BC013573 Homo sapi
721	45	3.4	1782	10	BC050802	BC050802 Mus muscu	794	45	3.4	2296	9	BC044946	BC044946 Homo sapi
722	45	3.4	1788	9	BC042092	BC042092 Homo sapi	795	45	3.4	2313	9	AB070026	AB070026 Macaca fa

796	45	3.4	2326	6	AX351139	AX351139 Sequence	869	45	3.4	3338	9	HSW803696	AL832388 Homo sapi
797	45	3.4	2353	5	BC053415	BC053415 Dario rer	870	45	3.4	3382	10	BC031718	BC031718 Mus muscu
798	45	3.4	2356	10	BC050243	BC050243 Mus muscu	871	45	3.4	3386	9	BC004191	BC004191 Homo sapi
799	45	3.4	2367	9	HSW801757	AL136789 Homo sapi	872	45	3.4	3393	6	AX167242	AX167242 Sequence
800	45	3.4	2372	9	BC042652	BC042652 Homo sapi	873	45	3.4	3404	5	BC044703	BC044703 Xenopus l
801	45	3.4	2373	10	BC031543	BC031543 Mus muscu	874	45	3.4	3406	9	BC048287	BC048287 Homo sapi
802	45	3.4	2388	9	AF115511	AF115511 Homo sapi	875	45	3.4	3415	10	AF361078	AF361078 Mus muscu
803	45	3.4	2411	9	BC007420	BC007420 Homo sapi	876	45	3.4	3420	9	BC038433	BC038433 Homo sapi
804	45	3.4	2416	9	BC032427	BC032427 Homo sapi	877	45	3.4	3423	10	BC010717	BC010717 Mus muscu
805	45	3.4	2432	10	BC050110	BC050110 Mus muscu	878	45	3.4	3448	10	BC046596	BC046596 Mus muscu
806	45	3.4	2433	10	BC011658	BC011658 Homo sapi	879	45	3.4	3500	9	BC030133	BC030133 Homo sapi
807	45	3.4	2443	9	BC019562	BC019562 Homo sapi	880	45	3.4	3503	10	BC042490	BC042490 Mus muscu
808	45	3.4	2445	9	BC040745	BC040745 Mus muscu	881	45	3.4	3552	9	BC036784	BC036784 Homo sapi
809	45	3.4	2466	3	AY058712	AY058712 Drosophi	882	45	3.4	3554	10	AF137367	AF137367 Mus muscu
810	45	3.4	2476	9	BC027910	BC027910 Homo sapi	883	45	3.4	3566	9	HSW803611	AL832330 Homo sapi
811	45	3.4	2508	5	LFT308118	AJ308118 Lampetra	884	45	3.4	3616	9	HSW804663	AL833330 Homo sapi
812	45	3.4	2516	10	BC037388	BC037388 Mus muscu	885	45	3.4	3717	3	AF384164	AF384164 Manduca s
813	45	3.4	2522	10	BC049158	BC049158 Mus muscu	886	45	3.4	3724	9	HSW804529	AL833218 Homo sapi
814	45	3.4	2528	8	AF126550	AF126550 Glycine m	887	45	3.4	3748	9	BC027942	BC027942 Homo sapi
815	45	3.4	2543	3	AY070710	AY070710 Drosophi	888	45	3.4	3766	9	HSW800878	AL110222 Homo sapi
816	45	3.4	2543	9	BC003656	BC003656 Homo sapi	889	45	3.4	3780	10	BC052316	BC052316 Mus muscu
817	45	3.4	2581	3	DDIGF138A	D12883 Dictyosteli	890	45	3.4	3848	9	HSW802401	BC032401 Homo sapi
818	45	3.4	2581	10	BC026392	BC026392 Mus muscu	891	45	3.4	3856	9	HSW805531	AL834437 Homo sapi
819	45	3.4	2606	10	BC023316	BC023316 Mus muscu	892	45	3.4	3888	10	BC052637	BC052637 Mus muscu
820	45	3.4	2628	9	HSW803071	BC032691 Homo sapi	893	45	3.4	3939	9	BC042431	BC042431 Homo sapi
821	45	3.4	2665	9	BC006136	BC006136 Homo sapi	894	45	3.4	3988	10	AB029066	AB029066 Mus muscu
822	45	3.4	2668	5	SSA293335	AJ293335 Salmo sai	895	45	3.4	4097	10	BC025565	BC025565 Mus muscu
823	45	3.4	2679	9	BC008198	BC008198 Homo sapi	896	45	3.4	4106	3	AY128421	AY128421 Drosophi
824	45	3.4	2682	9	BC002473	BC002473 Homo sapi	897	45	3.4	4115	6	BD012818	BD012818 Ys68, a n
825	45	3.4	2683	10	BC052924	BC052924 Mus muscu	898	45	3.4	4115	6	BD012822	BD012822 Ys68, a n
826	45	3.4	2685	9	HSW803071	AL713788 Homo sapi	899	45	3.4	4115	6	BD123392	BD123392 Ys68 gene
827	45	3.4	2687	3	DME312133	AJ312133 Drosophi	900	45	3.4	4115	6	BD123396	BD123396 Ys68 gene
828	45	3.4	2687	9	BC028993	BC028993 Homo sapi	901	45	3.4	4158	9	BC050289	BC050289 Homo sapi
829	45	3.4	2688	9	BC021087	BC021087 Homo sapi	902	45	3.4	4165	9	HSW804627	AL833334 Homo sapi
830	45	3.4	2690	9	BC011891	BC011891 Homo sapi	903	45	3.4	4343	5	AF159906	AF159906 Lapeinis h
831	45	3.4	2719	9	BC012479	BC012479 Homo sapi	904	45	3.4	4355	10	BC053033	BC053033 Mus muscu
832	45	3.4	2728	9	BC022218	BC022218 Homo sapi	905	45	3.4	4365	6	AX352580	AX352580 Sequence
833	45	3.4	2733	9	BC041092	BC041092 Homo sapi	906	45	3.4	4365	6	AX700120	AX700120 Sequence
834	45	3.4	2763	9	AK095553	AK095553 Homo sapi	907	45	3.4	4365	6	AF114168	AF114168 Mus muscu
835	45	3.4	2776	10	AB076079	AB076079 Mus muscu	908	45	3.4	4463	10	BC018533	BC018533 Mus muscu
836	45	3.4	2783	10	BC039183	BC039183 Homo sapi	909	45	3.4	4751	3	AF134171	AF134171 Dictyoste
837	45	3.4	2804	10	S69407	S69407 Edg=endogli	910	45	3.4	4820	10	BC052716	BC052716 Mus muscu
838	45	3.4	2815	9	BC001790	BC001790 Homo sapi	911	45	3.4	4879	5	BC047162	BC047162 Xenopus l
839	45	3.4	2815	9	BC018727	BC018727 Homo sapi	912	45	3.4	5012	3	AY069824	AY069824 Drosophi
840	45	3.4	2836	6	ARI170129	ARI170129 Sequence	913	45	3.4	5076	9	AB062750	AB062750 Homo sapi
841	45	3.4	2836	6	ARI170130	ARI170130 Sequence	914	45	3.4	5078	10	BC052172	BC052172 Mus muscu
842	45	3.4	2836	6	BD069549	BD069549 Novel car	915	45	3.4	5840	9	BC035609	BC035609 Homo sapi
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844	45	3.4	2836	9	BC006575	BC006575 Homo sapi	917	45	3.4	6157	6	AX348614	AX348614 Sequence
845	45	3.4	2840	10	BC052769	BC052769 Mus muscu	918	45	3.4	6674	10	AB029291	AB029291 Mus muscu
846	45	3.4	2850	9	BC034737	BC034737 Homo sapi	919	45	3.4	6702	9	AF378756	AF378756 Homo sapi
847	45	3.4	2884	9	HSW800612	AL096720 Homo sapi	920	45	3.4	6931	9	HSW803520	AL832213 Homo sapi
848	45	3.4	2887	9	AF100752	AF100752 Homo sapi	921	45	3.4	7034	6	BD012825	BD012825 Ys68, a n
849	45	3.4	2887	9	BC020217	BC020217 Homo sapi	922	45	3.4	7034	6	BD123399	BD123399 Ys68 gene
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852	45	3.4	2911	9	BC020264	BC020264 Homo sapi	925	45	3.4	14803	3	AC116959	AC116959 Dictyoste
853	45	3.4	2937	9	BC008857	BC008857 Homo sapi	926	45	3.4	18567	2	AC018319	AC018319 Drosophi
854	45	3.4	2973	10	BC006077	BC006077 Mus muscu	927	45	3.4	33569	3	AC115685	AC115685 Dictyoste
855	45	3.4	3014	9	BC024695	BC024695 Homo sapi	928	45	3.4	36188	3	AC115608	AC115608 Dictyoste
856	45	3.4	3036	9	AF090896	AF090896 Homo sapi	929	45	3.4	40753	3	BFY18367	BFY18367 Branchiosto
857	45	3.4	3042	3	AY069826	AY069826 Drosophi	930	45	3.4	44621	9	AP001873	AP001873 Homo sapi
858	45	3.4	3137	9	BC000235	BC000235 Homo sapi	931	45	3.4	47340	9	AC069387	AC069387 Homo sapi
859	45	3.4	3149	10	BC040763	BC040763 Mus muscu	932	45	3.4	48876	10	AL928841	AL928841 Mouse DNA
860	45	3.4	3157	10	BC037118	BC037118 Mus muscu	933	45	3.4	49306	3	AC115606	AC115606 Dictyoste
861	45	3.4	3178	9	HSW802265	AL137531 Homo sapi	934	45	3.4	56028	2	AC101223	AC101223 Mus muscu
862	45	3.4	3179	9	BC018509	BC018509 Homo sapi	935	45	3.4	57538	3	AC115682	AC115682 Dictyoste
863	45	3.4	3183	9	BC044242	BC044242 Homo sapi	936	45	3.4	60648	5	AL672044	AL672044 Zebratfish
864	45	3.4	3241	3	AY121624	AY121624 Drosophi	937	45	3.4	64707	3	AC115607	AC115607 Dictyoste
865	45	3.4	3266	9	BC040945	BC040945 Homo sapi	938	45	3.4	66877	2	AC116062	AC116062 Rattus no
866	45	3.4	3299	9	BC038294	BC038294 Homo sapi	939	45	3.4	67632	2	AC105102	AC105102 Homo sapi
867	45	3.4	3301	10	BC029098	BC029098 Mus muscu	940	45	3.4	69966	9	AL391804	AL391804 Human DNA
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RESULT 3
AY069529
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster LD24634 full insert cDNA.
AY069529.1 GI:17862393
FLI_CDNA.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1210)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J.,
Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K.,
Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
Direct Submission
Submitted (10-DEC-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
2 (bases 1 to 1210)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
and Celniker, S.
Direct Submission
Submitted (22-JAN-2003) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu.
Location/Qualifiers
1. .1210
/organism="Drosophila melanogaster"
/mol_type="mRNA"
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KLNARSVPFEAKVQLDDIGCDIILKGLVHKKEKVEKRLIGFNGATLKSIELL
TDCVTVQGNVTVSALGPYKGLQOVRDVLVETMNNVHTPIYNTIKALMIKELMKDPLRAN
EDWSRFLPKPKNKINISKEQPKYKKQKQKVFPPSPQSPESKVDVQOLASGEVFLNQEQK
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LIKANKKARSS"
BASE COUNT 379 a 287 c 336 g 208 t
ORIGIN
Query Match 3.6%; Score 48; DB 3; Length 1210;
Best Local Similarity 100.0%; Pred. No. 6.1e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1279 CQTGTAAAAA 1326
Db 1161 CQTGTAAAAA 1208
RESULT 4
AY153819
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 1522)
AUTHORS
Mahajan, P.B. and Tagliani, L.
TITLE
Maize Rad23 genes and uses thereof
JOURNAL
Patent: US 6235972-A 1 22-MAY-2001;
FEATURES
Location/Qualifiers
source
1. .1522
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BASE COUNT 430 a 375 c 370 g 347 t
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Best Local Similarity 100.0%; Pred. No. 6.2e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1279 CQTGTAAAAA 1326
Db 1455 CQTGTAAAAA 1502
RESULT 5
AR243792
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 2227)
AUTHORS
Komatsoulis, G., Rosen, C.A., Ruben, S.M., Duan, R.D., Moore, P.A.,
Shi, Y., Lafleur, D.W., Wei, Y.-F., Ni, J., Florence, K.A., Young, P.,
Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H. and
Mucenski, M.
TITLE
Secreted protein HNF20
JOURNAL
Patent: US 6476195-A 30 05-NOV-2002;
FEATURES
Location/Qualifiers
source
1. .2227
/organism="unknown"
BASE COUNT 544 a 539 c 553 g 21 others
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Best Local Similarity 100.0%; Pred. No. 6.5e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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2179 CCGTGTAAAAA 2877 bp mRNA linear PRI 11-DEC-2001
BC018933 Homo sapiens, clone IMAGE:4111094, mRNA, partial cds.
BC018933 ACCESSION
BC018933.1 GI:17511952
Homo sapiens (human)
Homo sapiens
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2877)
Strausberg, R.
Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hgr.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.I., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McLooney, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantrop, S., Thomas, P.J.,
Tiongson, E.B., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILML at: http://image.llnl.gov
Series: IRAL Plate: 20 Row: C Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
FEATURES             Location/Qualifiers
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RKEPVHYVTEGAYRMLQEDQSLTCGSGAGTKENTKKVIOVLARVASSPGK
RKEPVHYVTEGAYRMLQEDQSLTCGSGAGTKENTKKVIOVLARVASSPGK
TYLLEKSRALQKDECSFHIFQLLGAGQLKADLLEPCSHYRFTNGPSSPGQ
KLCRLGLGVDFSRALTPRKIVGRDYVQAKTEQADFALEALAKATYERFRWL
LRLNLRDRSQRQASFGILDIAGFEI FOLNSPQLCINTYKELQFNHTFVLE
LRLNLRDRSQRQASFGILDIAGFEI FOLNSPQLCINTYKELQFNHTFVLE
QEEYQREIPATFLDGLDLPCLDIERPANPPQLLALDEECWFFKATDKSFEKV
AQEGGCHKPFRPHLRQADFSLVHYAGKYDYKANWLMQMDPLNDNVALLHST
DRLTAETWKVEGIVGLGVSSLDGPPGPRGRMFKTVGLQYKESLSRLMATLSNT

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NPSEVRCIVPNHEKRAKLEPRVLVDQRCNGVLEIGIRICQGFNRLIFQEFQRQRYE
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DIIVSQALAAAGHILARAFQKQKQOQSAIRVMOENCAAYLKLHQMWRWLTQVKKPLL
QVTRQDEVLOQARQELQVQELQOQSAIRVMOENCAAYLKLHQMWRWLTQVKKPLL
AAEETRGLAARQKQELVLELVSEARVGEBCSRQMTQKRLQHQIQHLEAHLEA
EGARQKQLEKVTTEAKIK"

BASE COUNT 676 a 853 c 900 g 448 t
ORIGIN

Query Match 3.6%; Score 48; DB 9; Length 2877;
Best Local Similarity 100.0%; Pred. No. 6,7e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1279 CGTGTAAAAA 2877 bp mRNA linear ROD 16-APR-2003
Mus musculus nardilysin, N-arginine dibasic convertase, NRD
convertase 1, mRNA (cDNA clone IMAGE:5346773), partial cds.
BC023786
BC023786 ACCESSION
BC023786.1 GI:23271733
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2969)
Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S.J., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sanchez, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2969)
Strausberg, R.
Direct Submission
Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hgr.nih.gov
Ahter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley,R.W., Bouffard,G.G., Breen,X., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantipop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAP Kit: 55 Row: h Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

Location/Qualifiers

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/lab_host="DH10B"
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/gene="Nr1d1"
/codon_start=1
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/protein_id="AAH23786.1"
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/db_xref="MGI:1201386"
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AETLKPEKKNIDTHARLEFWRMYSAHYMTLVQSKETLDTLEKVTETPSOEPN
NLGPKNFSLHTDFTDPAPNKLYRVPIRKIKHALTITWALPPQQOYRNVKPLHYSW
LVHGEKGSILSLYRKKNALALFGNGETGFQNSTYSVFSITLTDGEVHFYEV
AHTVQYLMQLKPEKRVFEIQIENEFYQRTDPEVYENMCMQLYPRQD
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NSWTEKPNFIDPLHLPALPAENKYLATDFLKAFCPCPEYPAKIVTQAQGLWYK
DNKFKTPKAVIRPHLISPLQKSAANVLFDFIVNLTNLAEPYEAADVQALEYKLV
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TRSLREYTMELLMWMEERPCFPLRTKOTGLYHYVPTCRNTSGILGFSVTGTOATK
YNSBETVDKTEEFLESPSEKIEMLTDAFTQVTLTKKECEDTHLGEVDNRNNEV
VTCQYLDRLAHIEALKSPSKSLVSWFKAHKPGSKMLSVHVGKGYKEEDGAP
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gene

CDS

Query Match 3.6%; Score 48; DB 10; Length 2969;
Best Local Similarity 100.0%; Pred. No. 6.7e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1279 CGTGTAAAAA...AAA 1326
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Db 2919 CGTGTAAAAA...AAA 2966
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BASE COUNT 869 a 654 c 681 g 765 t

ORIGIN

Query Match 3.6%; Score 48; DB 10; Length 2969;
Best Local Similarity 100.0%; Pred. No. 6.7e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1279 CGTGTAAAAA...AAA 1326
|||||

Db 2919 CGTGTAAAAA...AAA 2966
|||||

RESULT 8

AX203306

LOCUS

DEFINITION

AX203306

Sequence 51 from Patent WO0153836.
112 bp DNA linear PAT 30-AUG-2001

VERSION AX203306.1 GI:15392677

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

Db

RESULT 9

PSGAMRA

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

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JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

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/ gene="GA"
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/ codon_start=1
/ protein_id="CAA46272.1"
/ db_xref="GI:20725"
/ db_xref="SPPREMBL:Q41016"
/ translation="MQTALTFAATITVVLTPPKSVSHLTIPFTKKTASRAPPRTYA
IKVAGNSDPATVNSAFVQLEACERFGGEACLAIDMTPEVKLOPERSNDAPKTA
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227
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/ replace=""
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Best Local Similarity 100.0%; Pred. No. 2.1e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAACAAAAA 1326
Db 522 GTGTAACAAAAA 568

RESULT 10
AF467914 679 bp mRNA linear VRT 02-FEB-2003
LOCUS
DEFINITION Danio rerio parvalbumin isoform 1d mRNA, complete cds.
ACCESSION AF467914
VERSION AF467914.1 GI:28194097
KEYWORDS
SOURCE
ORGANISM Danio rerio (zebrafish)
REFERENCE
AUTHORS Hsiao,C.D., Tsai,W.Y. and Tsai,H.J.
TITLE Molecular cloning and developmental expression of parvalbumin genes
in zebrafish
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 679)
AUTHORS Hsiao,C.D., Tsai,W.Y. and Tsai,H.J.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-2002) Institute of Fisheries Science, 1 Roosevelt
Rd. 4 Sec. National Taiwan University, Taipei 106, Taiwan
FEATURES
source
1. .679
/ organism="Danio rerio"
/ mol_type="mRNA"
/ db_xref="taxon:7955"
28. .357
/ note="Ca2+ buffer; pvalb1d"
/ codon_start=1
/ product="parvalbumin isoform 1d"
/ protein_id="AAO33400.1"
/ db_xref="GI:28194098"
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BASE COUNT 208 a 151 c 153 g 167 t
ORIGIN

Query Match 3.5%; Score 47; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 619 GTGTAACAAAAA 665

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IKVAGNSDPATVNSAFVQLEACERFGGEACLAIDMTPEVKLOPERSNDAPKTA
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227
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Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAACAAAAA 1326
Db 594 GTGTAACAAAAA 640

RESULT 11
I03321 688 bp ss-DNA linear PAT 21-MAY-1993
LOCUS
DEFINITION Sequence 12 from Patent US 4886747.
ACCESSION I03321
VERSION I03321.1 GI:270715
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 688)
AUTHORS Derynck,R.M.A. and Goeddel,D.V.
TITLE Nucleic acid encoding TGF-beta and its uses
JOURNAL Patent: US 4886747-A 12 12-DEC-1989;
Genentech, Inc.; South San Francisco, CA
FEATURES
Location/Qualifiers
source
1. .688
/ organism="unknown"
BASE COUNT 240 a 137 c 138 g 173 t
ORIGIN

Query Match 3.5%; Score 47; DB 6; Length 688;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAACAAAAA 1326
Db 594 GTGTAACAAAAA 640

RESULT 12
BC053374 899 bp mRNA linear PRI 09-JUN-2003
LOCUS
DEFINITION Homo sapiens cDNA clone IMAGE:6169687, partial cds.
ACCESSION BC053374
VERSION BC053374.1 GI:31419639
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Fukayota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 899)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Pahay,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blackesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE human and mouse cDNA sequences
JOURNAL human and mouse cDNA sequences
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 899)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

```


REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lari, C.P., Legaspi, R.,
 Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgueon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 115 Row: n Column: 13
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 485570.

FEATURES
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/note="Vector: pCMV-SPORT6"
BASE COUNT 335 a 107 c 158 g 299 t
ORIGIN

Query Match 3.5%; Score 47; DB 9; Length 899;
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 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA
 DB 820 GTGTAAAAA

RESULT 13
 LOCUS AX478009
 DEFINITION Sequence 19 from Patent WO0244390.
 ACCESSION AX478009
 VERSION AX478009.1 GI:22217015
 KEYWORDS
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1
 Cahoon, E.B., Cahoon, R.E., Klein, T.M., Rafalski, A.J. and Sakai, H.
 Floral development genes
 Patent: WO 0244390-A 19 06-JUN-2002;
 E. I. du Pont de Nemours and Company (US)
 Location/Qualifiers
 1. .902
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /db_xref="taxon:4577"
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Query Match 3.5%; Score 47; DB 6; Length 902;

Best Local Similarity 100.0%; Pred. No. 2.3e-15;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA
 DB 822 GTGTAAAAA

RESULT 14
 LOCUS HST000210
 DEFINITION Homo sapiens mRNA full length insert cDNA clone EUROIIMAGE 712308.
 ACCESSION AL079309
 VERSION AL079309.1 GI:5102753
 KEYWORDS FLI_CDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Auffray, C., Ansorge, W., Ballabio, A., Estivill, X., Gibson, K.,
 Lehrach, H., Poustka, A. and Lundeberg, J.
 The European IMAGE consortium for integrated Molecular analysis of
 human gene transcripts
 Unpublished
 2 (bases 1 to 956)
 Bassi, M.T., Banfi, S., Riboni, M., Ballabio, A. and Borsani, G.
 Direct Submission
 Submitted (15-JUN-1999) Telethon Institute of Genetics and Medicine
 (TIGEM), Via Olgettina 58, 20132 Milano, ITALY. Tel: +39-02-215601
 Fax: +39-02-21560220 WWW site: <http://www.tigem.it> e-mail
 enquires: bassi@tigem.it, borsani@tigem.it
 EURO-IMAGE Consortium Contact: Auffray C
 CNRS UPR 420 - Genetique Moleculaire et Biologie du Developement
 IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8
 94801 Villejuif Cedex, FRANCE
 Tel: +33-1-49 58 34 98
 Fax: +33-1-49 58 35 09
 e-mail: auffray@infobiogen.fr
 This clone is available royalty-free through IMAGE Consortium
 Distributors.
 IMPORTANT: This sequence represents the full insert of this IMAGE
 cDNA clone. No attempt has been made to verify whether this
 corresponds to the full-length of the original mRNA from which it
 was derived.

FEATURES
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1. .956
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE cDNA clone 712308"
/clone_lib="NCI_CGAP_GCB1"
BASE COUNT 296 a 205 c 146 g 309 t
ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 2.3e-15;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA
 DB 910 GTGTAAAAA

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 DEFINITION Homo sapiens, clone IMAGE:5204063, mRNA, partial cds.
 ACCESSION BC027909
 VERSION BC027909.1 GI:20379883
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 981)
Strausberg, R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Laric, P., Legaspi, R., Maduro, O.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>
Series: IRAX Plate: 49 Row: f Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES
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BASE COUNT 320 a 248 c 181 g 232 t
ORIGIN
Query Match 3.5%; Score 47; DB 9; Length 981;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1280 GTGTAA 1326
Db 880 GTGTAA 926

Search completed: November 7, 2003, 18:41:27
Job time : 5055 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 15:40:45 ; Search time 399 Seconds

(without alignments)

8971.065 Million cell updates/sec

Title: US-10-024-806-1

Perfect score: 1326

Sequence: 1 gcgcggagcttccaaagccc.....aaaaaaaaaaaaaaaaaaaa 1326

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N Geneseq_19Jun03.*

Rank	ID	Score	Match	Length	DB	ID	Description
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3	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*	48	3.6	2227	21	AAZ26365	Human secreted pro
4	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*	48	3.6	2227	22	AAH34842	Human colon cancer
5	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*	48	3.6	2227	25	ACCS0729	Human secreted pro
6	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*	48	3.6	2227	25	ABZ71405	Secreted protein-e
7	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*	47	3.5	112	22	NAZ23329	Human prostate can
8	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*	47	3.5	380	23	ABV58152	Human prostate exp

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	48	3.6	1522	21	AAZ01230	Maize Rad23 protein
3	48	3.6	2227	21	AAZ26365	Human secreted pro
4	48	3.6	2227	22	AAH34842	Human colon cancer
5	48	3.6	2227	25	ACCS0729	Human secreted pro
6	48	3.6	2227	25	ABZ71405	Secreted protein-e
7	47	3.5	112	22	NAZ23329	Human prostate can
8	47	3.5	380	23	ABV58152	Human prostate exp

Human prostate exp	384	23	ABV57927
Human polynucleoti	429	22	AAI91141
Human prostate exp	439	23	ABV48477
Corn FI homologue	902	24	AAZ42244
Soybean stress res	939	25	ABX78363
Human secreted pro	1015	20	AAZ00713
Human secreted pro	1140	21	AAC59279
Human secreted pro	1201	21	AAZ37044
Human cDNA SEQ ID	1371	22	ABA06561
Human polynucleoti	1371	24	ABV83898
cDNA encoding nove	1428	22	AAZ40837
Human extracellular	1505	25	AAI51962
Secreted protein g	2057	22	AAF72803
Pig transforming g	2639	19	AAV52934
Pig TGF-beta-3 S	2669	15	AAQ56925
Entire porcine tra	2671	11	AAQ03303
cDNA sequence enco	2676	11	AAQ02819
Human cancer assoc	2968	21	AAZ78190
Human colon cancer	2968	22	AAH34408
Human secreted pro	2968	22	AAF32706
Human normal ovari	4186	20	AAZ41320
Human prostate exp	194	23	ABV48180
Human prostate exp	198	23	ABV56955
Human prostate exp	211	23	ABV59290
Human prostate exp	223	23	ABV57510
Human prostate exp	246	23	ABV58026
Human prostate exp	284	23	ABV55380
Human breast cance	287	22	AAZ4917
Bovine ESR associa	292	25	ABZ47011
Human prostate exp	309	23	ABV56871
Bovine ESR associa	317	25	ABX38201
T23 cDNA. Oryza s	347	13	AAQ27482
Human prostate exp	357	23	ABV56577
Human immune/haema	358	22	AAK63837
Human polynucleoti	371	22	AAI82880
Human prostate exp	371	23	ABV18394
Bovine ESR associa	383	25	ABX40401
Human polynucleoti	392	23	ABV48356
Human prostate exp	401	22	AAI87524
Human polynucleoti	403	22	AAI87330
Human prostate exp	406	23	ABV19885
Human polynucleoti	411	22	AAI91834
Human polynucleoti	414	22	AAI83063
Human polynucleoti	414	22	AAI91762
Human polynucleoti	418	22	AAI86360
Bovine ESR associa	418	25	ABX45485
Human prostate exp	419	23	ABV58161
Human prostate exp	439	23	ABV57512
Human prostate exp	448	23	ABV58275
Human prostate exp	496	23	ABV59232
Human prostate exp	501	23	ABV59092
Human prostate exp	506	23	ABV56904
Human prostate exp	519	23	ABV58031
Human secreted pro	524	23	ABV55409
Arabidopsis thalia	530	21	AAZ97036
Human prostate exp	535	25	ABX57417
Human adult T-cell	550	23	ABV57531
Human prostate exp	567	22	AAZ89704
Human colon cancer	586	23	ABV56303
Clone H905.107. H	593	21	AAI6257
Human secreted pro	742	18	AAV00437
Human secreted pro	743	22	AAZ23920
Human secreted pro	760	23	ABV29481
Human musculoskele	773	20	AAZ37388
Human cDNA encodin	773	22	AAZ35650
Human novel protei	773	22	AAZ26849
cDNA encoding nove	773	25	AAZ16751
Human secreted pro	809	21	ABX58638
Human colon cancer	809	22	AAH33266
Secreted protein-e	809	25	ABZ73377
Human secreted pro	809	25	ABZ66985
Human secreted pro	828	24	AAZ33814

82	46	3.5	890	20	AA04376	Human secreted pro	155	46	3.5	3003	23	ABX71423	Human nucleic acid
83	46	3.5	901	24	AB199659	Mouse ischaemic co	156	46	3.5	3281	22	AA08389	Human secreted pro
c 84	46	3.5	951	22	AA526859	Human cDNA encodin	157	46	3.5	3344	16	AAQ80228	Rat NDF clone 22 D
c 85	46	3.5	1014	21	AA526164	Human secreted pro	158	46	3.5	3376	22	AA560774	Human cancer agent
c 86	46	3.5	1065	25	AB113321	Breast specific re	159	46	3.5	3436	22	AA500767	Human B7-H3 cDNA c
c 87	46	3.5	1097	21	AA116195	Human prostate can	160	46	3.5	3436	22	AA500767	Human secreted pro
c 88	46	3.5	1164	24	AB054448	Human ovarian anti	161	46	3.5	3513	22	AB082683	TRIO like gene SEQ
c 89	46	3.5	1170	21	AA234331	cDNA encoding huma	162	46	3.5	3513	25	ACC46003	Human TRIO-like ge
c 90	46	3.5	1218	24	AA45834	Human secreted pro	163	46	3.5	3521	24	AA96406	Human caderin fam
c 91	46	3.5	1244	22	AAH33206	Human colon cancer	164	46	3.5	5120	25	ACC44839	Mouse LTRP-4 short
c 92	46	3.5	1282	24	AB567784	Human receptors an	165	46	3.5	5440	25	ACC44838	Mouse LTRP-4 long
c 93	46	3.5	1542	21	AA966669	DNA encoding a hum	166	46	3.5	6153	22	AAH18670	Human cDNA sequenc
c 94	46	3.5	1577	21	AA080569	Human secreted pro	167	46	3.5	6410	25	ABZ33706	Human colon tumour
c 95	46	3.5	1637	24	AA172316	Human transporter	168	46	3.5	6791	18	AA783319	Mouse receptor ME2
c 96	46	3.5	1660	21	AA297136	Human secreted pro	169	46	3.5	10195	18	AA783320	Mouse receptor ME2
c 97	46	3.5	1699	22	AA781789	Human secreted pro	170	45	3.4	188	24	ABL38026	Human colon tumour
c 98	46	3.5	1699	25	ACC50677	Human secreted pro	171	45	3.4	190	23	ABV20053	Human prostate exp
c 99	46	3.5	1757	22	AAH78964	Human D-HSP70 cDNA	172	45	3.4	193	22	AAK55174	Human immune/haema
c 100	46	3.5	1758	22	AA050563	Human secreted pro	173	45	3.4	198	23	ABV56528	Human prostate exp
c 101	46	3.5	1771	21	AA211662	Human breast and o	174	45	3.4	202	21	AA098563	Human colon cancer
c 102	46	3.5	1781	20	AA220104	Wheat serine palmi	175	45	3.4	209	23	ABV58765	Human prostate exp
c 103	46	3.5	1818	24	AB054937	Human ovarian anti	176	45	3.4	217	25	ABX30207	Human GDP-mannose
c 104	46	3.5	1820	20	AA200434	Human secreted pro	177	45	3.4	233	22	AAH31389	Human secreted pro
c 105	46	3.5	1843	22	AAH33289	Human colon cancer	178	45	3.4	255	25	ABX31005	Human GDP-mannose
c 106	46	3.5	1844	19	AAV24018	Human BHF1 coding	179	45	3.4	260	23	ABV58104	Human prostate exp
c 107	46	3.5	1872	24	ABN85798	Human phospholipas	180	45	3.4	272	23	ABV18469	Human prostate exp
c 108	46	3.5	2002	24	AB544409	Human hydroxymethy	181	45	3.4	274	22	AAH33782	Human colon cancer
c 109	46	3.5	2002	25	ABX93299	cDNA encoding huma	182	45	3.4	276	25	ABX32152	Human GDP-mannose
c 110	46	3.5	2018	22	AA45091	Human secreted pro	183	45	3.4	293	22	AAH71507	Human cervical can
c 111	46	3.5	2029	20	AA219897	Human foetal kidne	184	45	3.4	302	21	AA098700	Human colon cancer
c 112	46	3.5	2058	21	AA077754	Human cancer assoc	185	45	3.4	304	24	ABQ54969	Human ovarian anti
c 113	46	3.5	2058	22	AA004175	Human Her-2/neu ov	186	45	3.4	308	24	ABL62070	Colon adenocarcino
c 114	46	3.5	2087	21	AA077500	Human ORFX ORF3055	187	45	3.4	308	24	ABL62809	Breast cancer rela
c 115	46	3.5	2112	24	ABX91996	Lung specific nucl	188	45	3.4	308	24	ABL62809	Breast cancer rela
c 116	46	3.5	2136	21	AA265065	Membrane-bound pro	189	45	3.4	319	23	ABV49812	Human prostate exp
c 117	46	3.5	2136	22	AA346038	Human DNA encoding	190	45	3.4	332	22	AAH70043	Human prostate exp
c 118	46	3.5	2136	22	AA44211	Human PRO1141 (UNQ	191	45	3.4	342	22	AAI83214	Human polynucleoti
c 119	46	3.5	2136	25	AC577796	Human cDNA encodin	192	45	3.4	345	23	ABV57023	Human polynucleoti
c 120	46	3.5	2136	25	ABX98266	Novel human secret	193	45	3.4	346	23	ABV54289	Human prostate exp
c 121	46	3.5	2136	25	ABX98768	Novel human secret	194	45	3.4	365	25	ABX40291	Bovine EST associa
c 122	46	3.5	2136	25	AC05813	Human secreted/tra	195	45	3.4	385	22	AAI90964	Human polynucleoti
c 123	46	3.5	2136	25	ABX97857	Human PRO polynucl	196	45	3.4	391	22	AAI82408	Human polynucleoti
c 124	46	3.5	2136	25	ABX80313	Novel human secret	197	45	3.4	395	22	AAI87795	Human polynucleoti
c 125	46	3.5	2136	25	ABX80817	Human secreted/tra	198	45	3.4	399	22	AAI88765	Human polynucleoti
c 126	46	3.5	2136	25	ABX81200	Novel human secret	199	45	3.4	399	23	ABV58210	Human prostate exp
c 127	46	3.5	2136	25	ABX90290	Human secreted/tra	200	45	3.4	407	23	ABV58185	Human prostate exp
c 128	46	3.5	2136	25	ABX77901	Human PRO polynucl	201	45	3.4	424	23	ABV55712	Human prostate exp
c 129	46	3.5	2136	25	ABX78641	Human PRO polynucl	202	45	3.4	426	22	AAI88632	Human polynucleoti
c 130	46	3.5	2136	25	ABX79497	Human secreted/tr	203	45	3.4	443	8	AA070773	Sequence encoding
c 131	46	3.5	2136	25	ABX75654	Human cDNA encodin	204	45	3.4	444	25	ABX36116	Bovine EST associa
c 132	46	3.5	2136	25	ABX76859	Human PRO polynucl	205	45	3.4	447	24	ABL93994	Arabidopsis thalia
c 133	46	3.5	2136	25	ABX64136	cDNA encoding huma	206	45	3.4	452	24	ABV95411	Human pancreatic c
c 134	46	3.5	2136	25	ABX16699	Human cDNA encodin	207	45	3.4	456	22	AAI83054	Human polynucleoti
c 135	46	3.5	2136	25	ABX17100	Human PRO polynucl	208	45	3.4	456	25	ABX44494	Bovine EST associa
c 136	46	3.5	2196	14	ABV59663	Human secreted pro	209	45	3.4	462	23	ABV57002	Human prostate exp
c 137	46	3.5	2196	24	ABV37650	Human cDNA #1 for	210	45	3.4	465	23	ABV48253	Human prostate exp
c 138	46	3.5	2235	22	AA084351	Corn clone CPR951	211	45	3.4	481	23	ABV58614	Human prostate exp
c 139	46	3.5	2248	21	AA059806	Human secreted pro	212	45	3.4	489	23	ABV23693	Human prostate exp
c 140	46	3.5	2263	24	AB054413	Human ovarian anti	213	45	3.4	489	23	ABV29562	Human prostate exp
c 141	46	3.5	2360	22	AA077734	Human secreted pro	214	45	3.4	524	21	AA096571	Noncoding region o
c 142	46	3.5	2457	22	AA033081	DNA encoding huma	215	45	3.4	550	23	ABV57072	Human prostate exp
c 143	46	3.5	2527	21	AA182234	Lung cancer associ	216	45	3.4	551	23	ABV56917	Human prostate exp
c 144	46	3.5	2534	22	AA050502	Human secreted pro	217	45	3.4	556	24	ABQ36996	Oligonucleotide fo
c 145	46	3.5	2611	24	AB576421	cDNA encoding huma	218	45	3.4	556	24	ABQ36997	Oligonucleotide fo
c 146	46	3.5	2625	21	AAZ91922	Human mahogany pro	219	45	3.4	584	23	ABV57816	Human prostate exp
c 147	46	3.5	2760	22	AA077710	Human secreted pro	220	45	3.4	595	21	AA081133	Human secreted pro
c 148	46	3.5	2837	19	AAV46317	Human secreted pro	221	45	3.4	595	22	AA01171	Fertilisation-inde
c 149	46	3.5	2837	22	AA098483	Human cDNA clone C	222	45	3.4	600	24	ABQ52494	Oligonucleotide fo
c 150	46	3.5	2892	19	AAV58361	Coding sequence fo	223	45	3.4	600	24	ABQ52495	Oligonucleotide fo
c 151	46	3.5	2897	19	AAV28411	Human GATA-6 trans	224	45	3.4	601	21	AAZ51740	Glycine max thiole
c 152	46	3.5	2897	25	AC056565	Human signalling p	225	45	3.4	638	24	ABQ49520	Oligonucleotide fo
c 153	46	3.5	2924	25	ABT23242	Seed development e	226	45	3.4	638	24	ABQ49521	Oligonucleotide fo
c 154	46	3.5	2996	24	ABZ58826	Human 32624 polype	227	45	3.4	640	24	ABV83665	Human breast speci

228	45	3.4	690	22	ABH33877	Human colon cancer	301	45	3.4	1436	25	ABX73434	Human novel polynu
229	45	3.4	691	20	AZ52929	Human prostate tum	302	45	3.4	1483	22	AS04152	Human ras converti
230	45	3.4	707	22	AS25840	Human CDNA encodin	303	45	3.4	1492	22	ACC00648	Zea mays oil trait
231	45	3.4	707	22	ABX73181	Human novel polynu	304	45	3.4	1504	24	ACC05498	Human ovarian anti
232	45	3.4	713	22	AS26603	Human CDNA encodin	305	45	3.4	1507	22	AA05541	Human secreted pro
233	45	3.4	713	22	ABX73944	Human novel polynu	306	45	3.4	1549	20	AA24921	Human ras carboxy-
234	45	3.4	740	19	AAV23915	Plant CCR enzyme D	307	45	3.4	1556	21	AA66427	Human secreted pro
235	45	3.4	740	19	AAV23915	Pine cinnamoyl-CoA	308	45	3.4	1583	22	AAH34904	Human colon cancer
236	45	3.4	740	20	AA06881	Pinus radiata CCR	309	45	3.4	1657	17	AA730360	Human p57 coding s
237	45	3.4	741	19	AAV23878	Plant CCR enzyme D	310	45	3.4	1659	22	AAK34941	Human haematologic
238	45	3.4	741	19	AAV206882	Pine cinnamoyl-CoA	311	45	3.4	1659	24	ABK83666	Human CDNA differe
239	45	3.4	741	21	AA67965	Pinus radiata CCR	312	45	3.4	1686	21	AA77763	Human cancer assoc
240	45	3.4	756	24	AA37828	Soybean KCP-like p	313	45	3.4	1694	20	AA707431	Homo sapiens secre
241	45	3.4	768	24	ABN99158	Arabidopsis thalia	314	45	3.4	1711	19	AAV43617	Human secreted pro
242	45	3.4	775	21	AA61277	Human secreted pro	315	45	3.4	1721	19	AAV63820	Human secreted pro
243	45	3.4	780	21	AA21763	Human breast and o	316	45	3.4	1728	12	AAV38990	Human receptor for
244	45	3.4	788	21	AA68003	Pinus radiata CCR	317	45	3.4	1767	22	AA529126	CDNA encoding for
245	45	3.4	826	16	AAQ79736	Flower style-speci	318	45	3.4	1767	24	AB568266	CDNA encoding huma
246	45	3.4	826	18	AA764553	Tomato S-ribonucle	319	45	3.4	1776	18	AA791744	Tobacco calcium/ca
247	45	3.4	844	22	AA502226	Soybean Wuschel (W	320	45	3.4	1779	21	AAZ65347	Human secreted pro
248	45	3.4	887	21	AA59297	Human secreted pro	321	45	3.4	1797	22	AAI64157	Maize defence-indu
249	45	3.4	895	22	AAH34628	Human colon cancer	322	45	3.4	1800	22	AA707579	Human secreted pro
250	45	3.4	907	22	ABK52046	CDNA encoding maiz	323	45	3.4	1821	19	AAV59590	Human secreted pro
251	45	3.4	909	21	AA79961	Human secreted pro	324	45	3.4	1835	20	AA27245	Human CLAR1 codin
252	45	3.4	921	19	AAV40521	Homo sapiens CH27	325	45	3.4	1859	21	AA81052	Human secreted pro
253	45	3.4	938	19	AAV27142	Novel haemopoietin	326	45	3.4	1877	21	AAZ99797	CDNA encoding a G-
254	45	3.4	938	21	AA46793	DNA encoding a mur	327	45	3.4	2035	8	AA70687	DNA encoding huma
255	45	3.4	938	22	AA04194	Murine haemopoieti	328	45	3.4	2059	24	AAZ38816	Human PSNA CDNA, P
256	45	3.4	941	4	AA30062	Sequence of a modi	329	45	3.4	2108	21	AA96570	A core 2 beta-1,6-
257	45	3.4	957	11	AA00441	Aequorin gene, Ae	330	45	3.4	2142	22	AAH31355	Human prostate pro
258	45	3.4	958	21	AA78018	Human cancer assoc	331	45	3.4	2143	23	ABV24475	Human prostate exp
259	45	3.4	958	22	AAH33258	Human colon cancer	332	45	3.4	2143	23	ABV24620	Human prostate exp
260	45	3.4	958	22	AA92253	Apoaequorin-encodi	333	45	3.4	2143	23	ABV24928	Human prostate exp
261	45	3.4	958	24	ABQ79813	Apoaequorin-encodi	334	45	3.4	2150	22	AAH81781	Human differential
262	45	3.4	958	24	ABQ79826	Apoaequorin-encodi	335	45	3.4	2198	21	AA23424	CDNA encoding huma
263	45	3.4	958	24	AA221188	Aequorea victoria	336	45	3.4	2260	22	AAI97914	Human neuroblastom
264	45	3.4	959	9	AA81534	pAQ440 aequorin ge	337	45	3.4	2260	22	AAI98068	Human neuroblastom
265	45	3.4	1018	25	ABX78394	Wheat stress respo	338	45	3.4	2326	22	AAH43381	CDNA sequence enco
266	45	3.4	1021	24	ABK66007	Rainbow trout CDNA	339	45	3.4	2381	21	AAI18106	Lung cancer associ
267	45	3.4	1041	21	AAFI6005	Human prostate can	340	45	3.4	2602	19	AAAI2416	CDNA encoding a hu
268	45	3.4	1054	25	ACC00688	Glycine max oil tr	341	45	3.4	2836	19	AAV40744	C. felis esterase,
269	45	3.4	1063	22	AA833256	DNA encoding huma	342	45	3.4	2836	19	AAV40745	C. felis esterase,
270	45	3.4	1077	22	AA827462	CDNA encoding nove	343	45	3.4	2836	19	AAV40745	Ctenocephalides fe
271	45	3.4	1091	22	AA897723	Maize ZmGn1-1 gl	344	45	3.4	2887	21	AA556703	Human transitional
272	45	3.4	1091	25	ABX95035	CDNA encoding maiz	345	45	3.4	3084	22	AA525910	Human CDNA encodin
273	45	3.4	1093	21	AA77825	Human cancer assoc	346	45	3.4	3084	25	ABX73251	Human novel polynu
274	45	3.4	1093	24	ABK50888	CDNA encoding muri	347	45	3.4	3288	22	AA05613	Human secreted pro
275	45	3.4	1095	21	AA77435	Human ORFX ORF2990	348	45	3.4	3288	22	AA05613	Human secretin-lik
276	45	3.4	1119	22	AA90638	Human TANGO 369 CD	349	45	3.4	3393	22	AA90612	Human secreted pro
277	45	3.4	1129	24	ABL50679	Human polynucleoti	350	45	3.4	3393	22	ABD05582	DNA encoding huma
278	45	3.4	1143	19	AAV59619	Human secreted pro	351	45	3.4	3393	24	AB52738	Human cancer assoc
279	45	3.4	1143	24	AB573606	Human CDNA #1 for	352	45	3.4	3397	21	AA78020	Human secreted pro
280	45	3.4	1159	22	AA502547	Human secreted pro	353	45	3.4	3397	22	AA78020	Human secreted pro
281	45	3.4	1178	24	ABV72167	Nucleotide sequenc	354	45	3.4	3465	20	AA89616	Human CDNA encodin
282	45	3.4	1186	24	ABK35838	CDNA sequence #229	355	45	3.4	3465	24	AA59247	Human polynucleoti
283	45	3.4	1212	20	AAK76499	Human WISP-3 prote	356	45	3.4	3465	24	ABA90916	Human secreted pro
284	45	3.4	1212	20	AAK76499	Human WISP-3 prote	357	45	3.4	3477	22	AA45120	Murine coding sequ
285	45	3.4	1233	21	AA71869	Human breast and o	358	45	3.4	4115	22	AAH19489	Murine coding sequ
286	45	3.4	1240	24	ABL01589	Human secreted pro	359	45	3.4	4115	22	AAH19493	Murine GABA-B rece
287	45	3.4	1263	24	AB574466	Maize peroxidase g	360	45	3.4	4365	25	ABA93497	Nucleotide sequenc
288	45	3.4	1266	21	AA76083	Human ORFX ORF1638	361	45	3.4	4365	25	AB268445	Human cell growth,
289	45	3.4	1267	21	AA77794	Human cancer assoc	362	45	3.4	4524	25	AB224701	M. sexta acetylcho
290	45	3.4	1280	21	AA74295	Human secreted pro	363	45	3.4	5554	25	ABV73333	Chemically treated
291	45	3.4	1293	24	AA563048	Cell death protect	364	45	3.4	6157	24	ABL70182	Signal transductio
292	45	3.4	1300	24	ABK34865	Human CDNA encodin	365	45	3.4	6157	24	ABK31225	Murine coding sequ
293	45	3.4	1303	22	AA329144	CDNA encoding for	366	45	3.4	7034	22	AAH19496	Human immune syste
294	45	3.4	1303	24	AB568284	CDNA encoding huma	367	45	3.4	7536	21	ABL33464	Human ORFX ORF2028
295	45	3.4	1307	25	AB234881	Coding sequence SE	368	45	3.4	8458	21	AACT6473	Human genomic DNA
296	45	3.4	1315	24	AB283451	Mouse MP-1 encodin	369	45	3.4	8711	22	AA526809	Human novel polynu
297	45	3.4	1340	25	AB276267	Human GENSET CDNA	370	45	3.4	8711	25	ABX74158	Human novel polynu
298	45	3.4	1405	25	ABX13973	Human Ras-like pro	371	44	3.3	50	25	ABQ77278	Oligo at primer.
299	45	3.4	1414	22	AAH35016	Human colon cancer	372	44	3.3	69	18	AA788081	3' portion of CDNA
300	45	3.4	1436	22	AA526093	Human CDNA encodin	373	44	3.3	69	18	AAV02148	Human secreted pro

C 520	44	3.3	220	25	ABX49357	Bovine EST associa	593	44	3.3	267	23	ABV56597	Human prostate exp
521	44	3.3	221	23	ABV19669	Human prostate exp	C 594	44	3.3	268	23	ABV38724	Human prostate exp
522	44	3.3	222	14	AAQ46071	Sequence downstre	C 595	44	3.3	269	23	ABV07492	Human prostate exp
523	44	3.3	222	22	AAQ46071	Downstream sequenc	C 596	44	3.3	271	22	AAAL16362	Human breast cance
C 524	44	3.3	222	24	ABZ08197	Human leukocyte de	C 597	44	3.3	272	22	AAAL12564	Human nervous syst
525	44	3.3	223	24	ABV55382	Human prostate exp	C 598	44	3.3	272	22	AAAL12612	Human breast cance
526	44	3.3	223	24	ABV55382	Human prostate exp	C 599	44	3.3	272	25	ABX41821	Bovine EST associa
C 527	44	3.3	223	25	ABX35502	Human RecQ protein	C 600	44	3.3	273	23	ABV56926	Human prostate exp
528	44	3.3	226	22	AAQ29055	Bovine EST associa	C 601	44	3.3	273	24	ABQ54673	Human ovarian anti
C 529	44	3.3	226	22	AAQ29055	cdNA encoding for	C 602	44	3.3	274	23	ABV58263	Human prostate exp
530	44	3.3	226	22	AAQ29055	Human cervical can	C 603	44	3.3	274	24	ABZ08581	Human leukocyte de
C 531	44	3.3	226	23	ABV05927	Human prostate exp	C 604	44	3.3	276	23	ABV58412	Human prostate exp
532	44	3.3	226	24	ABZ08680	Human prostate exp	C 605	44	3.3	276	25	ABX44966	Bovine EST associa
533	44	3.3	226	24	ABZ08680	Human leukocyte de	C 606	44	3.3	277	23	ABV57365	Human prostate exp
C 534	44	3.3	228	25	ABX58195	cdNA encoding huma	C 607	44	3.3	277	25	ABX37131	Bovine EST associa
535	44	3.3	228	25	ABX58195	Bovine EST associa	C 608	44	3.3	277	25	ABX47508	Bovine EST associa
536	44	3.3	229	23	ABV57008	Human lung tumour	C 609	44	3.3	278	22	AAH69999	Human cervical can
537	44	3.3	229	23	ABV57008	Human prostate exp	C 610	44	3.3	278	23	ABV55135	Human prostate exp
538	44	3.3	229	24	ABX38188	cdNA encoding clon	C 611	44	3.3	280	23	ABV58623	Human prostate exp
539	44	3.3	229	25	ACAL0517	Human lung cancer-	C 612	44	3.3	281	21	AAQ00286	Human colon cancer
540	44	3.3	229	25	ABX99468	Lung cancer therap	C 613	44	3.3	281	23	ABV35976	Human prostate exp
541	44	3.3	230	22	AAH33118	Human colon cancer	C 614	44	3.3	282	23	ABV47775	Human prostate exp
542	44	3.3	230	22	AAH33118	Human prostate exp	C 615	44	3.3	283	23	ABV61303	Human prostate exp
543	44	3.3	230	23	ABV57305	Human prostate exp	C 616	44	3.3	285	22	AAAL34854	Human musculoskele
544	44	3.3	230	23	ABV57305	Human prostate exp	C 617	44	3.3	285	23	ABV18565	Human prostate exp
545	44	3.3	230	25	ABX45059	Human prostate exp	C 618	44	3.3	285	25	ABX57842	cdNA encoding nove
546	44	3.3	232	22	AAH33358	Bovine EST associa	C 619	44	3.3	286	25	ABX48177	Bovine EST associa
547	44	3.3	232	22	AAH33358	Human colon cancer	C 620	44	3.3	287	24	ABL87079	Human ovarian can
548	44	3.3	232	22	AAH33358	Human prostate exp	C 621	44	3.3	287	25	ABT22943	Breast cancer mark
549	44	3.3	233	22	AAQ29129	cdNA encoding for	C 622	44	3.3	287	25	ABX40723	Bovine EST associa
550	44	3.3	233	22	AAQ29129	Human colon cancer	C 623	44	3.3	289	14	AAQ53450	Sequence of the 3'
551	44	3.3	234	23	ABV57891	cdNA encoding huma	C 624	44	3.3	289	22	AAAL16073	Human breast cance
C 552	44	3.3	235	23	ABV60929	Human prostate exp	C 625	44	3.3	289	22	AAAL16073	Human breast cance
553	44	3.3	236	23	ABV56953	Human prostate exp	C 626	44	3.3	289	23	ABV49828	Human polynucleoti
C 554	44	3.3	236	25	ABT22889	Breast cancer mark	C 627	44	3.3	289	20	AAZ13376	Human prostate exp
555	44	3.3	237	25	ABV07534	Human prostate exp	C 628	44	3.3	291	20	AAZ13376	Human gene express
C 556	44	3.3	237	25	ABV07534	Human prostate exp	C 629	44	3.3	291	24	ABK44641	Human prostate exp
557	44	3.3	238	22	ABX60314	Bovine EST associa	C 630	44	3.3	291	24	ABK44641	cdNA encoding colo
558	44	3.3	239	22	ABAL1191	Human cancer agent	C 631	44	3.3	291	25	ABX36078	Bovine EST associa
559	44	3.3	239	22	ABAL1191	Human nervous syst	C 632	44	3.3	291	25	ABX48529	Bovine EST associa
C 560	44	3.3	239	25	ABX46273	Human prostate exp	C 633	44	3.3	292	19	AAV21153	3' nucleotide port
561	44	3.3	239	25	ABX46273	Bovine EST associa	C 634	44	3.3	292	23	ABV49135	Human prostate exp
C 562	44	3.3	240	18	AAAT76782	Bovine EST associa	C 635	44	3.3	293	22	AAAL25205	Human breast cance
563	44	3.3	240	18	AAAT76782	Staphylococcus aur	C 636	44	3.3	294	22	AAK93729	Human cdna 3'-end
C 564	44	3.3	241	23	ABV58851	Human prostate exp	C 637	44	3.3	294	22	ABV56381	Human prostate exp
565	44	3.3	241	25	ABX40612	Human prostate exp	C 638	44	3.3	294	25	ABZ54909	Aspergillus oryzae
C 566	44	3.3	241	25	ABX40612	Bovine EST associa	C 639	44	3.3	295	22	AAQ29052	cdNA encoding for
567	44	3.3	241	25	ABX40612	Bovine EST associa	C 640	44	3.3	295	23	ABV19977	Human prostate exp
C 568	44	3.3	242	22	AAAL25805	Bovine EST associa	C 641	44	3.3	295	24	ABX68192	cdNA encoding huma
569	44	3.3	242	25	ABX38052	Human breast cance	C 642	44	3.3	296	22	AAAL16259	cdNA encoding huma
C 570	44	3.3	243	23	ABV56639	Bovine EST associa	C 643	44	3.3	296	22	AAAL16259	Human breast cance
571	44	3.3	243	25	AAAL25909	Human prostate exp	C 644	44	3.3	299	22	ABL87398	Human breast cance
C 572	44	3.3	247	22	AAH71353	Human cervical can	C 645	44	3.3	300	22	AAH70049	Human ovarian can
573	44	3.3	247	23	AAH71353	Human prostate exp	C 646	44	3.3	300	25	ABX41086	Human cervical can
C 574	44	3.3	248	23	ABV60876	Human prostate exp	C 647	44	3.3	303	23	ABV19295	Human prostate exp
575	44	3.3	250	23	ABV59115	Human prostate exp	C 648	44	3.3	303	23	ABV49738	Human prostate exp
C 576	44	3.3	252	23	ABV13586	Human prostate exp	C 649	44	3.3	304	22	ABZ29128	cdNA encoding for
577	44	3.3	252	22	AAH82206	Human prostate exp	C 650	44	3.3	304	23	ABV19428	Human prostate exp
C 578	44	3.3	256	22	AAH82206	Rat differential t	C 651	44	3.3	304	23	ABV55655	Human prostate exp
579	44	3.3	256	23	ABV52378	Human prostate exp	C 652	44	3.3	304	24	ABV58268	cdNA encoding huma
C 580	44	3.3	257	25	ABX44248	Bovine EST associa	C 653	44	3.3	305	23	ABV58043	Human prostate exp
581	44	3.3	257	23	ABV59128	Human prostate exp	C 654	44	3.3	306	24	ABZ08725	Human leukocyte de
C 582	44	3.3	257	23	ABV59128	Human prostate exp	C 655	44	3.3	307	22	ABZ29073	cdNA encoding for
583	44	3.3	258	22	AAAL19074	Bovine EST associa	C 656	44	3.3	307	23	ABV48143	Human prostate exp
C 584	44	3.3	258	22	AAAL19074	Human breast cance	C 657	44	3.3	307	24	ABV68213	cdNA encoding huma
585	44	3.3	259	25	ABX56911	Human prostate exp	C 658	44	3.3	308	25	ABX42505	Bovine EST associa
C 586	44	3.3	259	25	ABX42088	Bovine EST associa	C 659	44	3.3	309	23	ABV44994	Human prostate exp
587	44	3.3	262	24	ABX55426	Human colon cancer	C 660	44	3.3	309	23	ABV49356	Human prostate exp
C 588	44	3.3	264	24	ABL87207	Human ovarian can	C 661	44	3.3	309	23	ABV57373	Human prostate exp
589	44	3.3	265	22	AAH71554	Human cervical can	C 662	44	3.3	310	22	ABV71505	Human cervical can
C 590	44	3.3	265	22	AAH71554	Human breast cance	C 663	44	3.3	310	23	ABL87211	Human ovarian can
591	44	3.3	266	23	ABV07596	Human prostate exp	C 664	44	3.3	311	24	ABL87180	Human prostate exp
592	44	3.3	267	22	AAQ60607	Human cancer agent	C 665	44	3.3	311	24	ABL87180	Human ovarian can
										312	25	ABX41150	Bovine EST associa

666	44	3.3	312	25	ABX43249	Bovine EST associa	C 739	44	3.3	352	23	ABV60857	Human prostate exp
667	44	3.3	313	25	ABX37505	Bovine EST associa	740	44	3.3	353	22	AAI80163	Human polynucleoti
668	44	3.3	314	22	AAQ29145	CDNA encoding for	741	44	3.3	354	22	AAI87541	Human polynucleoti
669	44	3.3	314	22	AAK61200	Human immune/haema	742	44	3.3	355	22	AAI81491	Human polynucleoti
670	44	3.3	314	23	ABV04305	Human prostate exp	C 743	44	3.3	355	25	ABX37780	Bovine EST associa
671	44	3.3	314	23	ABV58492	Human prostate exp	C 744	44	3.3	355	25	ABX49592	Bovine EST associa
672	44	3.3	314	24	ABV58492	CDNA encoding huma	745	44	3.3	356	23	ABV43201	Human prostate exp
673	44	3.3	315	22	AAH71521	Human cervical can	746	44	3.3	357	22	AAI87170	Human polynucleoti
674	44	3.3	315	22	ABV54312	Human prostate exp	747	44	3.3	358	23	ABV48348	Human prostate exp
675	44	3.3	317	23	ABV51715	Human prostate exp	748	44	3.3	359	23	ABV18767	Human prostate exp
676	44	3.3	317	23	ABV58763	Human prostate exp	749	44	3.3	359	23	ABV56960	Human prostate exp
677	44	3.3	317	25	ABX37534	Bovine EST associa	C 750	44	3.3	359	24	ABQ85688	Arabidopsis thalia
678	44	3.3	318	23	ABV56059	Human prostate exp	C 751	44	3.3	360	22	AAI20475	Human breast cance
679	44	3.3	318	24	ABT10735	Human breast cance	752	44	3.3	360	23	ABV59054	Human prostate exp
680	44	3.3	318	22	ABV55820	Bovine EST associa	C 753	44	3.3	360	24	ABQ85662	Arabidopsis thalia
681	44	3.3	320	22	AAI84550	Human polynucleoti	754	44	3.3	361	22	AAI87168	Human polynucleoti
682	44	3.3	320	22	ABV49069	Human prostate exp	755	44	3.3	361	22	AAI88713	Human polynucleoti
683	44	3.3	320	22	AAI08164	Human breast cance	756	44	3.3	361	23	ABV56706	Human prostate exp
684	44	3.3	321	23	ABV34590	Human prostate exp	C 757	44	3.3	361	24	ABL85588	Human ovarian can
685	44	3.3	321	23	ABV43446	Human prostate exp	758	44	3.3	362	22	AAI83208	Human polynucleoti
686	44	3.3	322	22	AAI19416	Human breast cance	C 759	44	3.3	362	25	ABX40225	Bovine EST associa
687	44	3.3	323	23	ABV60996	Human prostate exp	C 760	44	3.3	363	23	ABV12992	Human prostate exp
688	44	3.3	323	25	ABX44970	Bovine EST associa	761	44	3.3	364	22	AAH34350	Human colon cancer
689	44	3.3	324	23	ABV57099	Human prostate exp	762	44	3.3	364	23	ABV56939	Human prostate exp
690	44	3.3	325	22	AAQ29049	CDNA encoding for	763	44	3.3	364	25	ABX44254	Bovine EST associa
691	44	3.3	325	24	ABQ86889	Bovine EST associa	764	44	3.3	365	22	AAI83450	Human polynucleoti
692	44	3.3	325	25	ABX43454	Human polynucleoti	765	44	3.3	365	22	AAI86853	Human polynucleoti
693	44	3.3	326	22	AAI90437	Human prostate exp	766	44	3.3	365	22	AAI87543	Human polynucleoti
694	44	3.3	327	23	ABV52133	Human prostate exp	767	44	3.3	365	23	AAI88393	Human polynucleoti
695	44	3.3	327	23	ABV49436	Human prostate exp	768	44	3.3	366	21	AAC98273	Human colon cancer
696	44	3.3	331	23	ABV56426	Human prostate exp	769	44	3.3	366	22	AAI82117	Human polynucleoti
697	44	3.3	331	25	AAH72555	Breast cancer mark	770	44	3.3	366	22	AAI87537	Human polynucleoti
698	44	3.3	332	22	AAH71330	Human cervical can	771	44	3.3	367	23	ABV19488	Human prostate exp
699	44	3.3	332	23	ABV13891	Human prostate exp	C 772	44	3.3	367	23	ABV54973	Human prostate exp
700	44	3.3	332	23	ABV49368	Human prostate exp	773	44	3.3	368	22	AAQ60046	Human cancer agent
701	44	3.3	332	23	ABV55846	Human prostate exp	774	44	3.3	368	22	AAI90378	Human polynucleoti
702	44	3.3	332	23	ABV56463	Human prostate exp	775	44	3.3	370	21	AAZ51574	Haematobia irritan
703	44	3.3	335	22	AAQ60452	Human cancer agent	776	44	3.3	370	22	AAI88518	Human polynucleoti
704	44	3.3	335	22	AAI19579	Human breast cance	777	44	3.3	370	22	AAK56906	Human immune/haema
705	44	3.3	335	22	AAI84803	Human polynucleoti	778	44	3.3	370	25	ABX41004	Bovine EST associa
706	44	3.3	337	23	ABV55706	Human prostate exp	779	44	3.3	372	9	AAH80489	Cowpea trypsin inh
707	44	3.3	337	23	ABV58905	Human prostate exp	780	44	3.3	372	22	AAI89007	Human polynucleoti
708	44	3.3	337	24	ABQ86019	Arabidopsis thalia	781	44	3.3	372	22	AAI91018	Human polynucleoti
709	44	3.3	337	25	ABX41811	Bovine EST associa	C 782	44	3.3	372	23	ABV37528	Human prostate exp
710	44	3.3	338	22	AAI80023	Human polynucleoti	C 783	44	3.3	373	25	ABX35671	Bovine EST associa
711	44	3.3	338	23	ABV48996	Human prostate exp	C 784	44	3.3	373	25	ABX38490	Bovine EST associa
712	44	3.3	338	23	ABV60873	Human prostate exp	785	44	3.3	374	22	AAI84577	Human polynucleoti
713	44	3.3	338	24	ABZ08610	Human leukocyte de	786	44	3.3	374	22	AAI84793	Human polynucleoti
714	44	3.3	339	23	ABV56910	Human prostate exp	787	44	3.3	374	22	AAI91055	Human polynucleoti
715	44	3.3	340	20	AAV89136	EST clone BR309	788	44	3.3	375	18	AAH84939	Human prostate pro
716	44	3.3	341	22	AAI83390	Human polynucleoti	789	44	3.3	375	20	AAK35869	CDNA encoding a pr
717	44	3.3	341	23	ABV49431	Human prostate exp	790	44	3.3	375	22	AAI90861	Human polynucleoti
718	44	3.3	343	22	AAI88988	Human polynucleoti	C 791	44	3.3	375	23	ABV44911	Human prostate exp
719	44	3.3	343	23	ABV60943	Human prostate exp	792	44	3.3	375	23	ABV58452	Human prostate exp
720	44	3.3	344	22	AAI85033	Human polynucleoti	C 793	44	3.3	375	25	ABX49849	Bovine EST associa
721	44	3.3	344	25	ABX47837	Bovine EST associa	794	44	3.3	376	22	AAI84760	Human polynucleoti
722	44	3.3	345	23	ABV07703	Human prostate exp	795	44	3.3	376	22	AAI87530	Human polynucleoti
723	44	3.3	345	23	AAI60689	Human prostate exp	796	44	3.3	376	23	ABV57109	Human prostate exp
724	44	3.3	346	22	AAI87483	Human polynucleoti	C 797	44	3.3	377	25	ABX44260	Bovine EST associa
725	44	3.3	346	22	AAI93468	Human polynucleoti	798	44	3.3	378	22	AAI82660	Human polynucleoti
726	44	3.3	347	22	AAI83215	Human polynucleoti	799	44	3.3	378	22	AAI83210	Human polynucleoti
727	44	3.3	347	22	AAI87559	Human polynucleoti	800	44	3.3	378	22	AAI90863	Human polynucleoti
728	44	3.3	347	25	ABX35931	Bovine EST associa	C 801	44	3.3	378	22	AAI90863	Sugarcane plant ge
729	44	3.3	347	25	ABX38206	Bovine EST associa	C 802	44	3.3	379	22	AAI20476	Human breast cance
730	44	3.3	349	22	ABQ85842	Arabidopsis thalia	803	44	3.3	380	22	AAI88350	Human polynucleoti
731	44	3.3	350	22	AAI82669	Human polynucleoti	804	44	3.3	380	22	AAK91627	Human cDNA 5'-end
732	44	3.3	350	24	ABQ85831	Arabidopsis thalia	805	44	3.3	380	22	AAK93551	Human cDNA clone r
733	44	3.3	350	24	ABQ54299	Human ovarian anti	806	44	3.3	380	23	ABV49790	Human prostate exp
734	44	3.3	351	22	ABX46565	Bovine EST associa	C 807	44	3.3	381	22	AAI86023	Human polynucleoti
735	44	3.3	351	22	AAI82851	Human polynucleoti	C 808	44	3.3	381	23	ABV14968	Human prostate exp
736	44	3.3	351	22	ABV55243	Human prostate exp	C 809	44	3.3	382	22	AAI82890	Human polynucleoti
737	44	3.3	351	24	ABQ85821	Arabidopsis thalia	810	44	3.3	382	22	AAI84706	Human polynucleoti
738	44	3.3	352	23	ABV56898	Human prostate exp	811	44	3.3	382	22	AAI87526	Human polynucleoti

812	44	3..3	382	22	AA187806	Human polynucleoti	C 885	44	3..3	396	24	ABL48777	Ovarian carcinoma
813	44	3..3	382	22	AA187942	Human polynucleoti	C 886	44	3..3	396	24	ABL48801	Ovarian carcinoma
C 814	44	3..3	382	22	ABV42927	Human prostate exp	C 887	44	3..3	396	24	ABL48812	Ovarian carcinoma
815	44	3..3	382	23	ABV49016	Human prostate exp	888	44	3..3	397	22	AA180153	Human polynucleoti
816	44	3..3	382	23	ABV54300	Human prostate exp	C 889	44	3..3	397	22	AA182664	Human polynucleoti
817	44	3..3	382	23	ABV56122	Human prostate exp	C 890	44	3..3	397	25	ABX48619	Bovine EST associa
818	44	3..3	383	22	AA188525	Human polynucleoti	891	44	3..3	398	22	AA188050	Human polynucleoti
C 819	44	3..3	383	22	AA188830	Human polynucleoti	892	44	3..3	398	22	AA188703	Human polynucleoti
820	44	3..3	383	22	AA188930	Human prostate exp	C 893	44	3..3	398	23	ABV34113	Human prostate exp
821	44	3..3	383	23	ABV34060	Human prostate exp	C 894	44	3..3	398	23	ABV42975	Human prostate exp
822	44	3..3	383	23	ABV57015	Human prostate exp	895	44	3..3	398	23	ABV58301	Human prostate exp
823	44	3..3	384	21	AA1801579	Human secreted pro	896	44	3..3	398	25	ABX46765	Bovine EST associa
824	44	3..3	384	21	AA183079	Human polynucleoti	897	44	3..3	399	17	AA130261	Cotton fibre cell-
825	44	3..3	384	22	AA185450	Human polynucleoti	898	44	3..3	399	17	AA13044	Cotton fibre-speci
C 826	44	3..3	384	22	AA188641	Human polynucleoti	899	44	3..3	399	18	AA170051	Cotton fibre speci
C 827	44	3..3	384	22	AA187011	Human cervical can	C 900	44	3..3	399	18	AA162620	Cotton fibre speci
828	44	3..3	384	23	ABV46128	Human prostate exp	C 901	44	3..3	399	21	AA182555	cDNA sequence a co
829	44	3..3	385	22	AA187439	Human polynucleoti	902	44	3..3	399	22	AA182053	Human polynucleoti
830	44	3..3	385	22	AA188475	Human polynucleoti	903	44	3..3	399	22	AA183196	Human polynucleoti
C 831	44	3..3	385	25	AA1861502	Arabidopsis thalia	904	44	3..3	399	22	AA183766	Human polynucleoti
832	44	3..3	386	22	AA183204	Human polynucleoti	905	44	3..3	399	22	AA193256	Human polynucleoti
833	44	3..3	386	22	AA189019	Human polynucleoti	C 906	44	3..3	399	25	ABX62704	Arabidopsis thalia
834	44	3..3	386	22	AA192181	Human polynucleoti	907	44	3..3	400	22	AA181389	Human polynucleoti
835	44	3..3	386	22	AA192904	Human polynucleoti	908	44	3..3	400	22	AA182922	Human polynucleoti
C 836	44	3..3	386	22	AA192904	Human polynucleoti	909	44	3..3	400	22	AA183631	Human polynucleoti
C 837	44	3..3	386	24	AB208601	Human leukocyte de	910	44	3..3	400	22	AA187341	Human polynucleoti
C 838	44	3..3	387	22	AA125102	Human breast cance	911	44	3..3	400	22	AA187360	Human polynucleoti
C 839	44	3..3	387	23	AA187769	Human prostate exp	912	44	3..3	400	22	AA187455	Human polynucleoti
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841	44	3..3	388	22	AA189390	Human polynucleoti	914	44	3..3	400	22	AA192151	Human polynucleoti
C 842	44	3..3	388	25	ABX41515	Bovine EST associa	915	44	3..3	400	23	ABV54560	Human prostate exp
C 843	44	3..3	389	22	AA120088	Human breast cance	916	44	3..3	400	23	ABV58615	Human prostate exp
844	44	3..3	389	22	AA120088	CDNA encoding for	917	44	3..3	401	22	AA187600	Human polynucleoti
845	44	3..3	389	22	AA188025	Human polynucleoti	918	44	3..3	401	22	AA187692	Human polynucleoti
846	44	3..3	389	22	AA188648	Human polynucleoti	C 919	44	3..3	401	25	ABX53255	Bovine EST associa
847	44	3..3	389	22	AA189111	Human polynucleoti	C 920	44	3..3	402	22	AA119713	Human breast cance
848	44	3..3	389	22	AA191234	Human polynucleoti	921	44	3..3	402	22	AA182881	Human polynucleoti
849	44	3..3	389	24	ABX68275	CDNA encoding huma	922	44	3..3	402	22	AA182950	Human polynucleoti
850	44	3..3	390	22	AA183046	Human polynucleoti	923	44	3..3	402	22	AA185111	Human polynucleoti
851	44	3..3	390	22	AA184812	Human polynucleoti	924	44	3..3	402	22	AAK56972	Human immune/haema
852	44	3..3	390	22	AA186998	Human polynucleoti	C 925	44	3..3	402	24	ABZ08435	Human leukocyte de
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854	44	3..3	390	23	ABV55403	Human prostate exp	927	44	3..3	403	22	AA182884	Human polynucleoti
855	44	3..3	391	22	AA183087	Human polynucleoti	928	44	3..3	403	22	AA183077	Human polynucleoti
856	44	3..3	391	22	AA186854	Human polynucleoti	929	44	3..3	403	22	AA187342	Human polynucleoti
857	44	3..3	391	22	AA187310	Human polynucleoti	930	44	3..3	403	22	AA190893	Human polynucleoti
858	44	3..3	391	22	AA187702	Human polynucleoti	931	44	3..3	404	22	AA183701	Human polynucleoti
859	44	3..3	392	22	AA187456	Human polynucleoti	932	44	3..3	404	22	AA184137	Human polynucleoti
860	44	3..3	392	22	AA188705	Human polynucleoti	933	44	3..3	404	22	AA187162	Human polynucleoti
861	44	3..3	392	23	ABV54346	Human prostate exp	934	44	3..3	404	22	AA189005	Human polynucleoti
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864	44	3..3	393	22	AA187824	Human polynucleoti	C 937	44	3..3	404	25	ABX62608	Arabidopsis thalia
C 865	44	3..3	393	25	ABX39417	Bovine EST associa	938	44	3..3	404	25	ABX38979	Bovine EST associa
C 866	44	3..3	394	22	AA184810	Human contig polyn	C 939	44	3..3	404	25	ABX45586	Bovine EST associa
867	44	3..3	394	23	ABV18659	Human prostate exp	940	44	3..3	405	22	AA183331	Human polynucleoti
868	44	3..3	394	23	ABV49244	Human prostate exp	941	44	3..3	405	22	AA184799	Human polynucleoti
869	44	3..3	394	23	ABV57207	Human prostate exp	942	44	3..3	405	22	AA187334	Human polynucleoti
870	44	3..3	394	23	ABV57930	Human prostate exp	943	44	3..3	405	22	AA187598	Human polynucleoti
C 871	44	3..3	394	25	ABX42549	Bovine EST associa	944	44	3..3	405	22	AA188052	Human polynucleoti
872	44	3..3	395	21	AA122339	Human secreted pro	945	44	3..3	406	22	AA187091	Human polynucleoti
873	44	3..3	395	22	AA181559	Human polynucleoti	946	44	3..3	406	22	AA187349	Human polynucleoti
874	44	3..3	395	22	AA185122	Human polynucleoti	C 947	44	3..3	406	23	ABV56001	Human prostate exp
875	44	3..3	395	22	AA186381	Human polynucleoti	948	44	3..3	406	23	ABV60840	Human prostate exp
C 876	44	3..3	396	22	AA184819	Human ovarian can	949	44	3..3	407	22	AA183065	Human polynucleoti
C 877	44	3..3	396	22	AA184819	Human ovarian can	950	44	3..3	407	22	AA183805	Human polynucleoti
C 878	44	3..3	396	22	AA184819	Human ovarian can	951	44	3..3	407	22	AA189211	Human polynucleoti
C 879	44	3..3	396	22	AA184819	Human ovarian can	952	44	3..3	407	22	AA189750	Human polynucleoti
C 880	44	3..3	396	24	ABT03086	Human ovarian can	C 953	44	3..3	407	23	ABV60716	Human prostate exp
C 881	44	3..3	396	24	ABT03094	Human ovarian can	954	44	3..3	408	22	AA189257	Human polynucleoti
C 882	44	3..3	396	24	ABT03118	Human ovarian can	955	44	3..3	408	22	AA191282	Human polynucleoti
C 883	44	3..3	396	24	ABT03129	Human ovarian can	C 956	44	3..3	408	23	ABV14972	Human prostate exp
C 884	44	3..3	396	24	ABT03129	Ovarian carcinoma	C 957	44	3..3	408	25	ABX41098	Bovine EST associa

958 44 3.3 409 22 AAI81346 Human polynucleoti
 959 44 3.3 409 22 AAI85121 Human polynucleoti
 960 44 3.3 409 22 AAI90784 Human polynucleoti
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 965 44 3.3 410 22 AAI81795 Human secreted pro
 966 44 3.3 410 23 ABV54332 Human prostate exp
 967 44 3.3 410 25 ABX74223 Aparagus cDNA enco
 968 44 3.3 410 25 ABX39273 Bovine EST associa
 969 44 3.3 411 22 AAI82241 Human polynucleoti
 970 44 3.3 411 22 AAI84864 Human polynucleoti
 971 44 3.3 411 22 AAI87361 Human polynucleoti
 972 44 3.3 411 22 AAI87378 Human polynucleoti
 973 44 3.3 411 22 AAI87998 Human polynucleoti
 974 44 3.3 411 22 AAI91179 Human polynucleoti
 975 44 3.3 412 22 AAI80754 Human polynucleoti
 976 44 3.3 412 22 AAI84848 Human polynucleoti
 977 44 3.3 412 22 AAI87374 Human polynucleoti
 978 44 3.3 412 22 AAI87443 Human polynucleoti
 979 44 3.3 412 22 AAI87923 Human polynucleoti
 980 44 3.3 412 23 ABV48550 Human prostate exp
 981 44 3.3 412 23 ABV54282 Human prostate exp
 982 44 3.3 412 23 ABV56372 Human prostate exp
 983 44 3.3 412 23 ABV56553 Human prostate exp
 984 44 3.3 412 23 ABV57988 Human prostate exp
 985 44 3.3 413 22 AAI82940 Human polynucleoti
 986 44 3.3 413 22 AAI85119 Human polynucleoti
 987 44 3.3 413 22 AAI85186 Human polynucleoti
 988 44 3.3 413 22 AAI89034 Human polynucleoti
 989 44 3.3 413 24 ABL49494 Sequence #96 used
 990 44 3.3 413 24 ABL77265 Human ovarian canc
 991 44 3.3 413 24 ABK30684 Plant dwarfing/stu
 992 44 3.3 415 22 AAI92174 Human polynucleoti
 993 44 3.3 416 22 AAI87993 Human polynucleoti
 994 44 3.3 416 25 ABX36081 Bovine EST associa
 995 44 3.3 416 25 ABX39419 Bovine EST associa
 996 44 3.3 417 20 AAZ24888 Human secreted pro
 997 44 3.3 417 23 ABV04722 Human prostate exp
 998 44 3.3 417 25 ACC50754 Human secreted pro
 999 44 3.3 417 25 ABZ71417 Secreted protein-e
 1000 44 3.3 418 22 AAI88540 Human polynucleoti

ALIGNMENTS

RESULT 1
 AAX28358 ID AAX28358 standard; DNA; 3375 BP.

AC AAX28358;
 DT 18-JUN-1999 (first entry)
 XX
 XX Human Stat6 coding sequence.

Stat6; Stat6b; human; signal transducers and activators of transcription;
 isoform: myeloid cancer; asthma; sarcoma; scleroderma; fibrotic disease;
 bone marrow fibrosis; AIDS; Stat6c; ss.

OS Homo sapiens.
 XX
 XX WO9910493-A1.
 PN
 XX
 PD 04-MAR-1999.

XX 27-AUG-1998; 98WO-US17821.
 XX
 XX 05-JAN-1998; 98US-0070397.
 PR
 XX 27-AUG-1997; 97US-0056075.
 XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Larochele WJ, Patel B, Pierce JH;
 PI WPI; 1999-214517/18.
 DR P-PSDB; AAY05223.
 XX
 XX New isoforms of Stat6 - having differential effects on the
 FT modulation of Stat6 activity in cells
 FT
 PS Disclosure; Page 79-83; 88pp; English.
 XX
 XX This sequence encodes human Stat6 (signal transducers and activators
 CC of transcription). The invention relates to attenuated and dominant
 CC negative isoforms of human Stat6. The detection and quantitation of DNA
 CC or mRNA encoding Stat6 and/or Stat6b and/or Stat6c can be used to detect
 CC differential expression of Stat6 isoforms in numerous diseases, including
 CC myeloid cancer, asthma, sarcoma, scleroderma, bone marrow fibrosis,
 CC fibrotic diseases and AIDS. The nucleic acids can be used to screen
 CC genomic or cDNA libraries or to identify complementary sequences. The
 CC identification of the genetic locus of the Stat6 gene can be used for
 CC detection of chromosomal aberrations and translocations involving the
 CC Stat6 gene. Antibodies against the isoforms can be used to detect the
 CC presence of Stat6 and/or Stat6b and/or Stat6c in a sample. Because of the
 CC variation of the roles of Stat6b and Stat6c in regulating gene
 CC transcription the isolated and purified forms can be used to study gene
 CC regulation and in screening assays for identifying drug candidates which
 CC may be used as agonists or antagonists. The two polypeptides may also be
 CC used in gene therapy protocols. In particular, Stat6b and/or Stat6c can
 CC therapeutically modulate the development and differentiation of B and
 CC T cells and can enhance IL-4 immunological function in immunocompromised
 CC individuals. Stat6 activation correlates with functional responses
 CC induced by interleukin-4 (IL-4), IL-13 and platelet-derived growth factor
 CC (PDGF). Stat6b when compared Stat6 is an attenuated regulator of gene
 CC transcription. Stat6c is a dominant negative regulator of gene
 CC transcription.
 XX
 XX Sequence 3375 BP; 802 A; 967 C; 943 G; 663 T; 0 other;
 SQ
 Query Match 3.8%; Score 50; DB 20; Length 3375;
 Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1277 TTGCTGTAAAAA
 Db 3318 TTGCTGTAAAAA
 RESULT 2
 AAD01230 ID AAD01230 standard; cDNA; 1522 BP.
 XX
 XX AAD01230;
 DT 04-OCT-2000 (first entry)
 XX
 XX Maize Rad23 protein #1 encoding cDNA.
 DE
 XX Rad23; maize; ATCC No: PTA-530; recombinant expression cassette; wheat;
 KW transgenic plant; soybean; sunflower; sorghum; canola; modulator; ss.
 XX
 XX Zea mays.
 OS
 XX Key Location/Qualifiers
 FH 58..1275
 FT CDS /*tag= a
 FT /product= "Maize Rad23 protein #1"
 FT /note= "Contained in ATCC No: PTA-530"
 XX
 XX WO200031268-A1.
 XX
 XX 02-JUN-2000.
 PD
 XX

PR 13-NOV-2001; 2001US-331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2003-029900/02.
XX P-PSDB; ABR00226.
XX
XX New human secreted proteins and nucleic acids, useful for detecting,
XX PT preventing, diagnosing, prognosticating, treating and/or ameliorating
XX PT e.g. gastrointestinal diseases and disorders, or cancers -
XX
XX Claim 21; Page 888-889; 1216pp; English.
XX
XX ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted
XX protein genes, and ABP00011-ABP00299 represent the proteins they encode.
XX CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The
XX CC invention also encompasses antibodies specific for the secreted proteins,
XX CC the use of the secreted proteins in drug screening, and recombinant
XX CC vectors and host cells comprising a nucleic acid of the invention. The
XX CC secreted proteins, nucleic acids encoding them, antibodies or antibody
XX CC fragments specific for the secreted proteins, and modulators of protein
XX CC activity are useful for diagnosing, treating, ameliorating or preventing
XX CC digestive disorders. Such conditions include disorders of the mouth,
XX CC oesophagus, stomach, small intestine, large intestine, liver, biliary
XX CC tract and pancreas, and include cancers of these organs and tissues. The
XX CC secreted proteins and their nucleic acids may also be used in the
XX CC treatment of immune disorders, inflammation, infection,
XX CC hyperproliferative disorders, and to promote wound healing. Nucleic acids
XX CC of the invention may be used for chromosome identification, chromosome
XX CC mapping, in gene therapy, for identifying individuals from minute
XX CC biological samples, as hybridisation probes, and as molecular weight
XX CC markers. The present sequence represents a human secreted protein-
XX CC encoding cDNA clone of the invention.
XX
XX Sequence 2227 BP; 544 A; 539 C; 553 G; 570 T; 21 other;
XX
XX Query Match 3.6%; Score 48; DB 25; Length 2227;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-07;
XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1279 CGTGTAAA 1326
XX DB 2179 CGTGTAAA 2226
XX
XX
XX RESULT 7
XX AAS23329
XX ID AAS23329 standard; cDNA; 112 BP.
XX AC AAS23329;
XX
XX DT 24-OCT-2001 (first entry)
XX
XX DE Human prostate cancer marker #51.
XX
XX KW Prostate cancer; human; cancer marker; metastasis; diagnostic;
XX KW therapeutic; immunogenic; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200153836-A2.
XX
XX PD 26-JUL-2001.
XX
XX PF 24-JAN-2001; 2001WO-US02318.
XX
XX PR 24-JAN-2000; 2000US-0178525.
XX PR 17-FEB-2000; 2000US-0183245.
XX PR 16-MAR-2000; 2000US-0190139.
XX PR 31-MAY-2000; 2000US-0208126.
XX PR 18-JUL-2000; 2000US-0219705.

PR 13-DEC-2000; 2000US-0255160.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege W, Monahan JB;
XX WPI; 2001-432912/46.
XX
XX Detecting and characterizing human prostate cancer comprises comparing
XX PT level of expression of marker in patient sample to normal level of
XX PT expression of marker in control non-prostate cancer sample -
XX
XX Claim 1; Page 875; 975pp; English.
XX
XX The invention relates to a method of assessing whether a patient is
XX CC afflicted with prostate cancer (PCA) comprising comparing the level of
XX CC expression of a marker in a patient sample to the normal level of marker
XX CC expression in a control non-PCA sample, where a significant difference
XX CC between marker expression in the patient sample and the normal level is
XX CC an indication that the patient is afflicted with PCA. The method can also
XX CC be used for: (1) monitoring the progression of PCA in a patient; (2)
XX CC assessing the efficacy of a test compound for inhibiting PCA in a
XX CC patient; (3) assessing the efficacy of a therapy for inhibiting PCA in a
XX CC patient; (4) selecting a composition for inhibiting PCA in a patient;
XX CC (5) inhibiting PCA in a patient comprising administering the selected
XX CC composition; (6) making an isolated hybridoma which produces an antibody
XX CC useful for carrying out (1) comprising immunising a mammal using the
XX CC marker, isolating splenocytes from the mammal, fusing the splenocytes
XX CC with an immortalised cell line and screening individual hybridomas for
XX CC production of an antibody which specifically binds the marker; (7) an
XX CC antibody produced by the hybridoma of (6); (8) assessing the prostate
XX CC cell carcinogenic potential of a test compound; (9) inhibiting PCA in a
XX CC patient at risk for developing PCA; and (10) determining whether PCA has
XX CC metastasised in a patient or assessing the aggressiveness or indolence
XX CC of PCA. AAS23279-AAS23379 represent the coding sequences of prostate
XX CC cancer markers used in the method of the invention.
XX
XX Sequence 112 BP; 78 A; 5 C; 13 G; 16 T; 0 other;
XX
XX Query Match 3.5%; Score 47; DB 22; Length 112;
XX Best Local Similarity 100.0%; Pred. No. 4.9e-07;
XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1280 GGTGTAAA 1326
XX DB 47 GGTGTAAA 93
XX
XX
XX RESULT 8
XX ABV58152
XX ID ABV58152 standard; cDNA; 380 BP.
XX AC ABV58152;
XX
XX DT 13-SEP-2002 (first entry)
XX
XX DE Human prostate expression marker cDNA 58143.
XX
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200160860-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 20-FEB-2001; 2001WO-US05171.
XX
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.

PS Claim 1; SEQ ID NO 11201; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and

CC the encoded proteins (AA000010-AA03910) that exhibit activity relating to

CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and

CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and

CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 429 BP; 180 A; 63 C; 65 G; 121 T; 0 other;

Query Match 3.5%; Score 47; DB 22; Length 429;

Best Local Similarity 100.0%; Pred. NO. 3.8e-07;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTCTAAAAA 1326

DB 147 GTGTAAAAA 193

RESULT 11

ABV48477

ID ABV48477 standard; cDNA; 439 BP.

XX

AC ABV48477;

XX

DT 17-SEP-2002 (first entry)

XX

XX Human prostate expression marker cDNA 48469.

XX

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.

XX

OS Homo sapiens.

XX

XX WO200160860-A2.

XX

XX 23-AUG-2001.

XX

XX 20-FEB-2001; 2001WO-US05171.

XX

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

XX Schlegel R, Endege WO, Monahan JE;

XX

XX WPI; 2001-662795/76.

XX

XX Novel isolated nucleic acid molecule associated with cancerous state of

FT prostate cells and correlating with presence of prostate cancer, useful

FT for detecting presence of prostate cancer, stage of prostate cancer -

XX

PS Claim 1; Page 9503; 11750pp; English.

XX

CC The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX

SQ Sequence 439 BP; 204 A; 81 C; 72 G; 82 T; 0 other;

Query Match 3.5%; Score 47; DB 23; Length 439;

Best Local Similarity 100.0%; Pred. NO. 3.7e-07;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA 1326

DB 131 GTGTAAAAA 177

RESULT 12

AAD42244

ID AAD42244 standard; cDNA; 902 BP.

XX

AC AAD42244;

XX

XX 04-NOV-2002 (first entry)

XX

DE Corn FT homologue cDNA from clone p0104.cabak14rb.

XX

XX Floral developmental protein; flowering locus T; APETALA3; transgenic;

KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;

KW sterility; plant growth; inflorescence architecture; plant morphology;

KW tissue culture; cell division; corn; gene; ss.

XX

OS Zea mays.

XX

XX Key Location/Qualifiers

FH 90..611

CDS /*tag= a

FT /product= "Corn FT homologue protein"

FT

XX

XX WO200244390-A2.

XX

XX 06-JUN-2002.

XX

XX 21-NOV-2001; 2001WO-US43750.

XX

XX 28-NOV-2000; 2000US-253415P.

XX

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX

XX Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;

XX

XX WPI; 2002-547703/59.

XX

XX P-PSDB; AAE25742.

XX

XX New floral developmental polypeptide having flowering locus T or Ap3

FT homology activity, useful for immunological screening of cDNA expression

FT libraries -

XX

PS Claim 6; Page 61; 88pp; English.

XX

CC The present invention relates to novel floral developmental proteins,

CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue

CC proteins and polynucleotides encoding such proteins. Floral developmental

CC polynucleotides are useful for transforming cells or for producing plants

CC by transforming the plant cells with the polynucleotides and regenerating

CC the plants from the transformed plant cells. Sequences of the invention

CC are useful for immunological screening of cDNA expression libraries. They

CC are also useful for creating transgenic plants. Polynucleotides of the

PS Disclosure; Page 89; 205pp; English.

XX The invention relates to isolated nucleic acids encoding plant stress
CC response proteins (including peptide-methionine sulfoxide
CC reductases) appearing as ABUS8148-ABUS9246 (or a protein 80% identical
CC to them) from Zea mays, Oryza sativa, Glycine max, or Triticum aestivum.
CC Also included are expression cassettes, transformed host cells,
CC transgenic plants/seeds, modulating the level of peptide-methionine
CC sulfoxide reductase in a plant and a computer system/data
CC processing system for identifying, analysing, or modelling a genetic
CC sequence. The plant nucleic acid is useful in developing strategies to
CC improve plant response to stress (e.g. drought, heat, radiation or
CC pathogen attack), engineering plants with increased disease and stress
CC resistance, manipulating DNA repair and recombination efficiency,
CC manipulating intracellular protein transport, and improving/protecting
CC grain flavour. The nucleic acids may also be used as probes or
CC amplification primers in the detection, quantitation or isolation of gene
CC transcripts, for recombinant expression of encoded polypeptides, as
CC immunogens in preparing or screening antibodies, and in sense or
CC antisense suppression of one or more genes in a host cell, tissue or
CC plant. The proteins may be used as immunogens or antigens to obtain
CC antibodies specifically immunoreactive with the protein, and in assays
CC for enzyme agonists or antagonists. The present sequence is a plant
CC stress response cDNA or fragment (EST, expressed sequence tag).
XX

XX Sequence 939 BP; 307 A; 149 C; 220 G; 263 T; 0 other;
SQ

Query Match 3.5%; Score 47; DB 25; Length 939;
Best Local Similarity 100.0%; Pred.No. 3.2e-07;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1280 GTGCTAAAAA 1326
|||
Db 886 GTGCTAAAAA 932

RESULT 14
AAX00713
ID AAX00713 standard; DNA; 1015 BP.
AC AAX00713;
XX
DT 25-MAR-1999 (first entry)
XX
XX
DE Human secreted protein gene 51 clone HAPN080.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
XX WO9842738-A1.
FN
XX
PD 01-OCT-1998.
XX
XX 19-MAR-1998; 98WO-US05311.
PF
XX 30-MAY-1997; 97US-0050937.
PR
XX 21-MAR-1997; 97US-0041276.
PR
XX 21-MAR-1997; 97US-0041277.
PR
XX 21-MAR-1997; 97US-0041281.
PR
XX 21-MAR-1997; 97US-0042344.
PR
XX 30-MAY-1997; 97US-0048069.
PR
XX 30-MAY-1997; 97US-0048094.
PR
XX 30-MAY-1997; 97US-0048095.
PR
XX 30-MAY-1997; 97US-0048096.
PR
XX 30-MAY-1997; 97US-0048099.

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 17:03:05 ; Search time 94 Seconds

(without alignments)

6226.320 Million cell updates/sec

Title: US-10-024-806-1

Perfect score: 1326

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Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	50	3.8	3375	4	US-09-511-625B-67
2	48	3.6	1522	3	US-09-413-574-1
3	48	3.6	2227	4	US-09-489-847-30
4	47	3.5	1201	4	US-09-461-325-36
5	47	3.5	2671	6	5168051-9
6	46	3.5	347	1	US-08-104-072B-2
7	46	3.5	530	4	US-09-461-325-28
8	46	3.5	593	3	US-09-385-982-262
9	46	3.5	1660	4	US-09-461-325-129
10	46	3.5	1872	4	US-09-801-052-1
11	46	3.5	2002	4	US-09-819-993-1
12	46	3.5	2136	4	US-09-996-243-302
13	46	3.5	2196	4	US-09-149-476-163
14	46	3.5	2235	4	US-09-569-804-20
15	46	3.5	2625	3	US-09-245-041-18
16	46	3.5	2837	2	US-08-993-228-11
17	46	3.5	2897	2	US-08-927-394-1
18	46	3.5	2897	4	US-09-016-434-1163
19	46	3.5	3715	4	US-09-234-245-1
20	45	3.4	740	2	US-08-713-000-8
21	45	3.4	740	2	US-08-975-316-8
22	45	3.4	740	3	US-09-211-710-8
23	45	3.4	740	4	US-09-615-192A-8
24	45	3.4	741	2	US-08-975-316-58
25	45	3.4	741	4	US-09-615-192A-58
26	45	3.4	788	4	US-09-615-192A-96
27	45	3.4	958	2	US-08-757-046A-5

28	45	3.4	958	3	US-09-447-208-5	Sequence 5, Appli
29	45	3.4	958	3	US-09-135-988-5	Sequence 5, Appli
30	45	3.4	958	3	US-09-277-716-5	Sequence 5, Appli
31	45	3.4	958	3	US-08-597-274A-5	Sequence 5, Appli
32	45	3.4	958	4	US-08-908-909-5	Sequence 5, Appli
33	45	3.4	958	4	US-09-609-161B-5	Sequence 5, Appli
34	45	3.4	958	4	US-08-990-103-5	Sequence 5, Appli
35	45	3.4	1075	3	US-08-400-006B-6	Sequence 6, Appli
36	45	3.4	1091	4	US-09-328-965-1	Sequence 1, Appli
37	45	3.4	1143	4	US-09-149-476-119	Sequence 119, App
38	45	3.4	1212	4	US-09-182-145-34	Sequence 34, Appl
39	45	3.4	1212	4	US-09-182-145-35	Sequence 35, Appl
40	45	3.4	1315	4	US-09-721-822A-10	Sequence 10, Appl
41	45	3.4	1483	3	US-09-262-749-1	Sequence 1, Appli
42	45	3.4	1728	3	US-08-985-950-7	Sequence 7, Appli
43	45	3.4	1728	4	US-09-546-049-7	Sequence 10, Appl
44	45	3.4	1776	3	US-08-655-352-10	Sequence 10, Appl
45	45	3.4	1776	4	US-09-358-016-10	Sequence 10, Appl
46	45	3.4	1776	4	US-09-257-825B-10	Sequence 10, Appl
47	45	3.4	1821	4	US-09-149-476-90	Sequence 90, Appl
48	45	3.4	1835	4	US-09-485-549-1	Sequence 1, Appli
49	45	3.4	2836	3	US-08-747-221B-24	Sequence 24, Appl
50	45	3.4	2836	3	US-08-005-051-24	Sequence 24, Appl
51	45	3.4	2836	3	US-09-005-051-26	Sequence 26, Appl
52	45	3.4	2836	3	US-09-005-051-26	Sequence 26, Appl
53	44	3.3	80	4	US-09-284-627-23	Sequence 23, Appl
54	44	3.3	105	4	US-08-153-051B-28	Sequence 28, Appl
55	44	3.3	120	1	US-08-060-952C-44	Sequence 44, Appl
56	44	3.3	120	2	US-08-151-477A-28	Sequence 28, Appl
57	44	3.3	120	3	US-08-819-867-58	Sequence 58, Appl
58	44	3.3	120	3	US-08-464-011B-44	Sequence 44, Appl
59	44	3.3	120	4	US-09-378-535-58	Sequence 58, Appl
60	44	3.3	120	4	US-08-481-190-15	Sequence 15, Appl
61	44	3.3	141	1	US-08-628-417-5	Sequence 11, Appl
62	44	3.3	141	3	US-08-737-078A-1	Sequence 1, Appli
63	44	3.3	141	5	PCT-US94-04706-1	Sequence 1, Appli
64	44	3.3	141	5	US-08-702-344-26	Sequence 26, Appl
65	44	3.3	216	1	US-08-686-878A-34	Sequence 34, Appl
66	44	3.3	216	4	US-09-175-928-34	Sequence 34, Appl
67	44	3.3	222	3	US-08-481-190-15	Sequence 15, Appl
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69	44	3.3	223	4	US-09-792-594-11	Sequence 11, Appl
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77	44	3.3	399	1	US-07-885-970A-13	Sequence 13, Appl
78	44	3.3	399	1	US-08-298-687A-13	Sequence 12, Appl
79	44	3.3	399	1	US-08-530-797-12	Sequence 12, Appl
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83	44	3.3	458	2	US-08-524-757-1	Sequence 1, Appli
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86	44	3.3	487	4	US-09-257-179-22	Sequence 22, Appl
87	44	3.3	540	4	US-09-313-434C-15	Sequence 15, Appl
88	44	3.3	554	4	US-09-696-169A-14	Sequence 14, Appl
89	44	3.3	568	1	US-08-582-257-20	Sequence 20, Appl
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92	44	3.3	570	1	US-08-298-687A-10	Sequence 10, Appl
93	44	3.3	570	1	US-08-298-829-10	Sequence 10, Appl
94	44	3.3	572	4	US-09-696-169A-12	Sequence 12, Appl
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96	44	3.3	609	2	US-08-530-797-9	Sequence 9, Appli
97	44	3.3	609	2	US-08-787-335-9	Sequence 9, Appli
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106 44 3.3 826 6 PCT-US95-06406A-21 Sequence 102, App
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234 44 3.3 1842 4 US-09-482-273-90 Sequence 90, Appli
235 44 3.3 1858 2 US-08-909-965C-11 Sequence 11, Appli
236 44 3.3 1878 4 US-09-465-558-39 Sequence 39, Appli
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246 44 3.3 1934 3 US-08-776-844-1 Sequence 1, Appli

C 393	43	3.2	350	1	US-08-171-385-14	Sequence 14, Appl	466	43	3.2	879	1	US-08-158-682A-1	Sequence 1, Appl
C 394	43	3.2	350	2	US-08-361-441B-14	Sequence 14, Appl	467	43	3.2	879	1	US-08-015-203-1	Sequence 1, Appl
C 395	43	3.2	356	2	US-08-520-678A-22	Sequence 22, Appl	468	43	3.2	882	2	US-08-909-965C-9	Sequence 9, Appl
C 396	43	3.2	356	3	US-08-897-126-22	Sequence 22, Appl	469	43	3.2	888	3	US-09-188-910-13	Sequence 13, Appl
C 397	43	3.2	427	4	US-09-461-325-107	Sequence 107, App	470	43	3.2	888	4	US-09-312-283C-13	Sequence 13, Appl
C 398	43	3.2	441	4	US-09-601-537-10	Sequence 10, Appl	471	43	3.2	898	4	US-09-857-556A-29	Sequence 29, Appl
C 399	43	3.2	467	2	US-08-841-349-18	Sequence 18, Appl	472	43	3.2	917	4	US-09-227-357-43	Sequence 43, Appl
C 400	43	3.2	470	3	US-09-020-956-102	Sequence 102, App	473	43	3.2	921	4	US-09-227-357-30	Sequence 30, Appl
C 401	43	3.2	470	3	US-09-030-607-102	Sequence 102, App	474	43	3.2	931	4	US-09-482-273-31	Sequence 31, Appl
C 402	43	3.2	470	4	US-09-439-313-102	Sequence 102, App	475	43	3.2	941	4	US-08-471-717-1	Sequence 1, Appl
C 403	43	3.2	470	4	US-09-352-616A-102	Sequence 102, App	476	43	3.2	941	4	US-09-205-258-186	Sequence 186, App
C 404	43	3.2	470	4	US-09-232-149A-102	Sequence 102, App	477	43	3.2	949	4	US-09-489-847-35	Sequence 35, Appl
C 405	43	3.2	472	4	US-09-203-258-130	Sequence 130, App	478	43	3.2	953	1	US-08-197-793-1	Sequence 1, Appl
C 406	43	3.2	474	3	US-08-516-859A-97	Sequence 97, Appl	479	43	3.2	953	1	US-08-636-176-1	Sequence 1, Appl
C 407	43	3.2	474	4	US-09-586-472-97	Sequence 97, Appl	480	43	3.2	953	5	PCT-US95-01618-1	Sequence 1, Appl
C 408	43	3.2	474	4	US-09-528-706-97	Sequence 97, Appl	481	43	3.2	960	3	US-09-248-335-57	Sequence 57, Appl
C 409	43	3.2	485	4	US-09-996-243-245	Sequence 245, App	482	43	3.2	967	3	US-09-248-335-51	Sequence 51, Appl
C 410	43	3.2	495	4	US-09-220-132-186	Sequence 186, App	483	43	3.2	972	1	US-07-915-934-1	Sequence 1, Appl
C 411	43	3.2	509	3	US-09-030-607-202	Sequence 202, App	484	43	3.2	972	1	US-08-325-743-1	Sequence 1, Appl
C 412	43	3.2	509	4	US-09-439-313-202	Sequence 202, App	485	43	3.2	972	4	US-09-549-831-5	Sequence 5, Appl
C 413	43	3.2	509	4	US-09-352-616A-202	Sequence 202, App	486	43	3.2	972	4	US-09-996-243-358	Sequence 358, App
C 414	43	3.2	509	4	US-09-232-149A-202	Sequence 202, App	487	43	3.2	974	2	US-08-504-459-13	Sequence 13, Appl
C 415	43	3.2	536	1	US-08-341-568-1	Sequence 1, Appl	488	43	3.2	975	4	US-09-381-488-6	Sequence 6, Appl
C 416	43	3.2	536	2	US-08-911-020-1	Sequence 1, Appl	489	43	3.2	985	4	US-03-322-409-25	Sequence 25, Appl
C 417	43	3.2	537	4	US-09-720-201A-4	Sequence 4, Appl	490	43	3.2	985	4	US-09-322-409-27	Sequence 27, Appl
C 418	43	3.2	551	4	US-09-996-243-166	Sequence 166, App	491	43	3.2	985	4	US-09-451-527-25	Sequence 25, Appl
C 419	43	3.2	552	4	US-09-461-325-111	Sequence 111, App	492	43	3.2	985	4	US-09-451-527-27	Sequence 27, Appl
C 420	43	3.2	569	4	US-09-461-325-44	Sequence 44, Appl	493	43	3.2	1001	1	US-08-728-259A-10	Sequence 10, Appl
C 421	43	3.2	570	4	US-09-996-243-407	Sequence 407, App	494	43	3.2	1001	2	US-08-473-486-10	Sequence 10, Appl
C 422	43	3.2	572	4	US-09-342-653-5	Sequence 5, Appl	495	43	3.2	1013	1	US-07-920-619-30	Sequence 30, Appl
C 423	43	3.2	577	3	US-09-385-982-203	Sequence 203, App	496	43	3.2	1013	1	US-08-086-410-23	Sequence 23, Appl
C 424	43	3.2	578	4	US-09-602-877A-95	Sequence 95, Appl	497	43	3.2	1013	1	US-08-314-586-30	Sequence 30, Appl
C 425	43	3.2	588	4	US-09-205-258-64	Sequence 64, Appl	498	43	3.2	1013	4	US-09-322-409-6	Sequence 6, Appl
C 426	43	3.2	593	4	US-09-904-615-59	Sequence 59, Appl	499	43	3.2	1013	4	US-09-322-409-8	Sequence 8, Appl
C 427	43	3.2	615	4	US-09-105-542A-2	Sequence 2, Appl	500	43	3.2	1013	4	US-09-451-527-6	Sequence 6, Appl
C 428	43	3.2	619	4	US-09-489-847-58	Sequence 58, Appl	501	43	3.2	1013	4	US-09-451-527-8	Sequence 8, Appl
C 429	43	3.2	630	1	US-08-185-414E-1	Sequence 1, Appl	502	43	3.2	1020	4	US-03-328-475C-43	Sequence 43, Appl
C 430	43	3.2	635	1	US-08-455-633A-35	Sequence 35, Appl	503	43	3.2	1023	1	US-08-252-966B-16	Sequence 16, Appl
C 431	43	3.2	635	1	US-08-416-336-5	Sequence 5, Appl	504	43	3.2	1023	4	US-09-229-947-38	Sequence 38, Appl
C 432	43	3.2	635	2	US-08-456-460C-35	Sequence 35, Appl	505	43	3.2	1029	4	US-09-216-393B-11	Sequence 11, Appl
C 433	43	3.2	635	5	PCT-US94-0535A-35	Sequence 35, Appl	506	43	3.2	1032	4	US-09-257-179-21	Sequence 21, Appl
C 434	43	3.2	636	4	US-09-594-506-27	Sequence 27, Appl	507	43	3.2	1036	4	US-09-205-258-86	Sequence 86, Appl
C 435	43	3.2	639	4	US-09-482-273-49	Sequence 49, Appl	508	43	3.2	1037	4	US-03-489-847-112	Sequence 112, App
C 436	43	3.2	644	4	US-09-996-243-282	Sequence 282, App	509	43	3.2	1039	4	US-09-464-535-23	Sequence 23, Appl
C 437	43	3.2	644	4	US-09-720-201A-6	Sequence 6, Appl	510	43	3.2	1046	1	US-08-361-467B-4	Sequence 4, Appl
C 438	43	3.2	664	4	US-09-904-615-66	Sequence 6, Appl	511	43	3.2	1046	1	US-08-484-332C-4	Sequence 4, Appl
C 439	43	3.2	674	4	US-09-620-405B-465	Sequence 465, App	512	43	3.2	1048	4	US-09-489-847-38	Sequence 38, Appl
C 440	43	3.2	674	4	US-09-433-828B-465	Sequence 465, App	513	43	3.2	1050	4	US-09-482-273-58	Sequence 58, Appl
C 441	43	3.2	674	4	US-09-604-287A-465	Sequence 465, App	514	43	3.2	1051	3	US-09-245-041-10	Sequence 10, Appl
C 442	43	3.2	685	4	US-09-227-357-66	Sequence 66, Appl	515	43	3.2	1066	1	US-08-157-101A-4	Sequence 4, Appl
C 443	43	3.2	688	6	5498694-3	Patent No. 5498694	516	43	3.2	1069	4	US-09-205-258-74	Sequence 74, Appl
C 444	43	3.2	700	4	US-09-152-060-26	Sequence 26, Appl	517	43	3.2	1098	3	US-09-248-335-35	Sequence 35, Appl
C 445	43	3.2	703	3	US-09-313-300-6	Sequence 6, Appl	518	43	3.2	1109	4	US-09-653-778B-1	Sequence 1, Appl
C 446	43	3.2	732	4	US-09-149-476-66	Sequence 66, Appl	519	43	3.2	1126	4	US-09-389-956-7	Sequence 7, Appl
C 447	43	3.2	742	1	US-07-847-010-12	Sequence 12, Appl	520	43	3.2	1129	4	US-09-227-357-40	Sequence 40, Appl
C 448	43	3.2	760	4	US-09-205-258-232	Sequence 232, App	521	43	3.2	1134	3	US-09-248-335-29	Sequence 29, Appl
C 449	43	3.2	773	4	US-09-149-476-20	Sequence 20, Appl	522	43	3.2	1144	4	US-09-904-615-20	Sequence 20, Appl
C 450	43	3.2	780	2	US-08-540-804-36	Sequence 36, Appl	523	43	3.2	1146	4	US-09-452-239-3	Sequence 3, Appl
C 451	43	3.2	780	3	US-08-590-399-36	Sequence 36, Appl	524	43	3.2	1147	1	US-08-665-716-1	Sequence 1, Appl
C 452	43	3.2	785	4	US-09-518-036-9	Sequence 9, Appl	525	43	3.2	1153	4	US-09-149-476-41	Sequence 41, Appl
C 453	43	3.2	785	4	US-09-205-258-73	Sequence 73, Appl	526	43	3.2	1181	4	US-09-149-476-310	Sequence 310, App
C 454	43	3.2	789	3	US-09-020-956-32	Sequence 32, Appl	527	43	3.2	1184	4	US-09-489-847-76	Sequence 76, Appl
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C 461	43	3.2	857	1	US-08-730-163-1	Sequence 1, Appl	534	43	3.2	1212	4	US-09-149-476-186	Sequence 186, App
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C 463	43	3.2	857	3	US-08-462-437-1	Sequence 1, Appl	536	43	3.2	1225	1	US-08-603-919-1	Sequence 1, Appl
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833	43	3.2	3060	4	US-09-996-243-504	Sequence 504, App	906	43	3.2	5125	3	US-09-031-563-4	Sequence 4, Appli
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835	43	3.2	3080	4	US-09-245-281-25	Sequence 25, Appl	908	43	3.2	5125	4	US-09-258-000-4	Sequence 4, Appli
836	43	3.2	3080	4	US-09-207-359B-25	Sequence 25, Appl	909	43	3.2	5232	4	US-08-972-927-1	Sequence 1, Appli
837	43	3.2	3080	4	US-09-340-620A-25	Sequence 25, Appl	910	43	3.2	5268	3	US-09-112-096-14	Sequence 14, Appl
838	43	3.2	3124	4	US-07-734-030-1	Sequence 1, Appli	911	43	3.2	5894	3	US-08-665-259-24	Sequence 24, Appl
839	43	3.2	3138	1	US-07-867-106-4	Sequence 4, Appli	912	43	3.2	5894	3	US-08-762-500-24	Sequence 24, Appl
840	43	3.2	3200	1	US-08-444-405-1	Sequence 1, Appli	913	43	3.2	5955	4	US-09-358-383C-14	Sequence 14, Appl
841	43	3.2	3200	1	US-08-384-850-1	Sequence 1, Appli	914	43	3.2	5962	6	5386025-5	Patent No. 5386025
842	43	3.2	3207	1	US-07-946-497-1	Sequence 1, Appli	915	43	3.2	5975	1	US-08-404-354B-1	Sequence 1, Appli
843	43	3.2	3207	1	US-08-483-322-1	Sequence 1, Appli	916	43	3.2	5975	1	US-08-314-083B-1	Sequence 1, Appli
844	43	3.2	3207	2	US-08-478-882-1	Sequence 1, Appli	917	43	3.2	5975	1	US-08-435-675B-1	Sequence 1, Appli
845	43	3.2	3238	3	US-08-123-334A-5	Sequence 5, Appli	918	43	3.2	5975	1	US-08-336-257A-3	Sequence 3, Appli
846	43	3.2	3238	5	PCT-US94-10080-5	Sequence 5, Appli	919	43	3.2	5975	3	US-08-884-599-1	Sequence 1, Appli
847	43	3.2	3242	4	US-09-493-914-2	Sequence 2, Appli	920	43	3.2	6525	3	US-08-762-500-74	Sequence 74, Appl
848	43	3.2	3255	4	US-09-996-243-378	Sequence 378, App	921	43	3.2	6671	1	US-08-280-443-1	Sequence 1, Appli
849	43	3.2	3275	4	US-09-370-838-151	Sequence 151, App	922	43	3.2	6671	1	US-08-457-459-1	Sequence 1, Appli
850	43	3.2	3300	4	US-09-336-643A-82	Sequence 82, Appl	923	43	3.2	6671	1	US-08-555-678-1	Sequence 1, Appli
851	43	3.2	3312	4	US-09-669-751-259	Sequence 259, App	924	43	3.2	6671	5	PCT-US95-02275-1	Sequence 1, Appli
852	43	3.2	3334	4	US-09-996-243-288	Sequence 288, App	925	43	3.2	7286	3	US-09-331-581-3	Sequence 3, Appli
853	43	3.2	3350	2	US-08-663-566A-1	Sequence 1, Appli	926	43	3.2	7859	1	US-07-854-596B-4	Sequence 4, Appli
854	43	3.2	3350	2	US-08-023-610-1	Sequence 1, Appli	927	43	3.2	7859	2	US-08-450-908B-15	Sequence 15, Appl
855	43	3.2	3350	2	US-08-288-065A-1	Sequence 1, Appli	928	43	3.2	7859	3	US-07-982-759F-15	Sequence 15, Appl
856	43	3.2	3350	2	US-08-362-240A-1	Sequence 1, Appli	929	43	3.2	7938	3	US-09-331-581-15	Sequence 14, Appl
857	43	3.2	3350	5	PCT-US95-10245-1	Sequence 1, Appli	930	43	3.2	8100	4	US-09-554-337-4	Sequence 4, Appli
858	43	3.2	3441	2	US-08-742-753-1	Sequence 1, Appli	931	43	3.2	9472	4	US-08-150-204B-96	Sequence 96, Appl
859	43	3.2	3736	2	US-08-480-473B-1	Sequence 1, Appli	932	43	3.2	9589	1	US-07-925-695-1	Sequence 1, Appli
860	43	3.2	3736	3	US-08-915-213-1	Sequence 1, Appli	933	43	3.2	9589	1	US-07-925-695-2	Sequence 2, Appli
861	43	3.2	3736	3	US-09-148-547-1	Sequence 1, Appli	934	43	3.2	9646	3	US-08-811-566-1	Sequence 1, Appli
862	43	3.2	3736	3	US-09-235-217-1	Sequence 1, Appli	935	43	3.2	9646	3	US-09-034-756-1	Sequence 1, Appli
863	43	3.2	3736	3	US-09-383-581-1	Sequence 1, Appli	936	43	3.2	9704	4	US-09-814-951A-3	Sequence 3, Appli
864	43	3.2	3736	5	PCT-US96-10251-1	Sequence 1, Appli	937	43	3.2	10660	2	US-08-267-803B-8	Sequence 8, Appli
865	43	3.2	3777	3	US-09-121-321-15	Sequence 15, Appl	938	43	3.2	10660	2	US-09-041-886-16	Sequence 16, Appl
866	43	3.2	3777	3	US-08-932-803A-15	Sequence 15, Appl	939	43	3.2	11517	1	US-07-920-281C-1	Sequence 1, Appli
867	43	3.2	3842	3	US-09-115-954-7	Sequence 7, Appli	940	43	3.2	11517	3	US-08-466-277-1	Sequence 1, Appli
868	43	3.2	3848	3	US-09-112-096-28	Sequence 28, Appl	941	43	3.2	12597	4	US-09-705-299-12	Sequence 12, Appl
869	43	3.2	3871	2	US-08-599-455B-3	Sequence 3, Appli	942	43	3.2	12980	3	US-08-811-566-5	Sequence 5, Appli
870	43	3.2	3871	3	US-09-069-781B-3	Sequence 3, Appli	943	43	3.2	12980	4	US-09-034-756-5	Sequence 5, Appli
871	43	3.2	3871	4	US-09-137-132-3	Sequence 3, Appli	944	43	3.2	15538	5	PCT-US92-06300-1	Sequence 1, Appli
872	43	3.2	3871	4	US-08-864-564A-3	Sequence 3, Appli	945	43	3.2	19557	4	US-09-816-093-3	Sequence 3, Appli
873	43	3.2	3871	4	US-09-094-410-3	Sequence 3, Appli	946	43	3.2	46718	4	US-09-816-093-3	Sequence 3, Appli
874	43	3.2	3871	4	US-08-708-123D-3	Sequence 3, Appli	947	42	3.2	75	2	US-08-776-944-13	Sequence 13, Appl
875	43	3.2	3871	4	US-08-583-153A-3	Sequence 3, Appli	948	42	3.2	646	4	US-09-288-143-22	Sequence 22, Appl
876	43	3.2	3871	4	US-08-570-142D-3	Sequence 3, Appli	949	42	3.2	756	2	US-08-530-165-1	Sequence 1, Appli
877	43	3.2	3871	4	US-08-638-524B-3	Sequence 3, Appli	950	42	3.2	859	3	US-09-247-373B-47	Sequence 47, Appl
878	43	3.2	3894	4	US-09-511-625B-3	Sequence 3, Appli	951	42	3.2	865	4	US-09-205-258-227	Sequence 227, App
879	43	3.2	3912	4	US-09-115-954-1	Sequence 1, Appli	952	42	3.2	943	4	US-09-149-476-35	Sequence 35, Appl
880	43	3.2	3927	4	US-09-293-238B-1	Sequence 1, Appli	953	42	3.2	991	4	US-09-344-529-3	Sequence 3, Appli
881	43	3.2	3933	1	US-08-199-776-1	Sequence 1, Appli	954	42	3.2	1037	4	US-09-344-529-1	Sequence 1, Appli
882	43	3.2	3933	3	US-08-663-731-1	Sequence 1, Appli	955	42	3.2	1035	2	US-08-580-545B-3	Sequence 3, Appli
883	43	3.2	3933	3	US-08-879-338-1	Sequence 1, Appli	956	42	3.2	1035	3	US-09-262-653A-3	Sequence 3, Appli
884	43	3.2	3933	5	PCT-US95-02044-1	Sequence 1, Appli	957	42	3.2	1035	3	US-08-867-484A-1	Sequence 1, Appli
885	43	3.2	4055	4	US-09-620-312D-706	Sequence 706, App	958	42	3.2	1035	4	US-09-834-659-1	Sequence 1, Appli
886	43	3.2	4072	3	US-09-245-041-16	Sequence 16, Appl	959	42	3.2	1035	4	US-09-760-892-1	Sequence 1, Appli
887	43	3.2	4086	4	US-09-702-705-1801	Sequence 1801, Ap	960	42	3.2	1035	4	US-09-834-656-1	Sequence 1, Appli
888	43	3.2	4086	4	US-09-736-457-1801	Sequence 1801, Ap	961	42	3.2	1094	4	US-09-522-714-1	Sequence 1, Appli
889	43	3.2	4121	4	US-09-601-537-9	Sequence 9, Appli	962	42	3.2	1139	4	US-09-590-454-13	Sequence 13, Appl
890	43	3.2	4137	4	US-09-499-964-2	Sequence 2, Appli	963	42	3.2	1400	4	US-09-245-281-40	Sequence 40, Appl
891	43	3.2	4419	4	US-09-620-312D-187	Sequence 187, App	964	42	3.2	1400	4	US-09-207-359B-40	Sequence 40, Appl
892	43	3.2	4456	4	US-09-095-443-1	Sequence 1, Appli	965	42	3.2	1400	4	US-09-340-620A-40	Sequence 40, Appl
893	43	3.2	4586	1	US-08-832-887-53	Sequence 53, Appl	966	42	3.2	1466	4	US-08-984-919A-10	Sequence 10, Appl
894	43	3.2	4586	2	US-08-832-877-53	Sequence 53, Appl	967	42	3.2	1466	4	US-08-984-919A-12	Sequence 12, Appl
895	43	3.2	4704	2	US-08-476-062A-52	Sequence 52, Appl	968	42	3.2	1472	3	US-08-781-420-10	Sequence 10, Appl
896	43	3.2	4765	3	US-08-936-135-21	Sequence 21, Appl	969	42	3.2	1472	3	US-08-781-420-12	Sequence 12, Appl
897	43	3.2	4780	3	US-08-936-135-23	Sequence 23, Appl	970	42	3.2	1472	4	US-08-874-102-10	Sequence 10, Appl
898	43	3.2	4843	3	US-08-986-485-1	Sequence 1, Appli	971	42	3.2	1472	4	US-08-874-102-12	Sequence 12, Appl
899	43	3.2	4880	3	US-09-031-563-1	Sequence 1, Appli	972	42	3.2	1472	4	US-09-006-595A-10	Sequence 10, Appl
900	43	3.2	4880	4	US-09-392-277-1	Sequence 1, Appli	973	42	3.2	1472	4	US-09-006-595A-12	Sequence 12, Appl
901	43	3.2	4880	4	US-09-258-000-1	Sequence 1, Appli	974	42	3.2	1607	6	5196333-3	Patent No. 5196333
902	43	3.2	4895	3	US-09-053-866-1	Sequence 1, Appli	975	42	3.2	1642	2	US-08-665-037-1	Sequence 1, Appli
903	43	3.2	4895	4	US-09-479-130-1	Sequence 1, Appli	976	42	3.2	1642	2	US-08-666-067-1	Sequence 1, Appli

RESULT 4

US-09-461-325-36
; Sequence 36, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: F2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; EARLIER FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 36
; LENGTH: 1201
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: n equals a.t.g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (48)
; OTHER INFORMATION: n equals a.t.g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (63)
; OTHER INFORMATION: n equals a.t.g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1201)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-461-325-36

Query Match 3.5%; Score 47; DB 4; Length 1201;
Best Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAGAAAAA 1326
DB 1131 GTGTAAGAAAAA 1177

RESULT 5

5168051-9
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO: 9
; LENGTH: 2671
5168051-9

Query Match 3.5%; Score 47; DB 6; Length 2671;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAGAAAAA 1326
DB 2577 GTGTAAGAAAAA 2623

RESULT 6

US-08-104-072B-2
; Sequence 2, Application US/08104072B
; Patent No. 5639948
; GENERAL INFORMATION:
; APPLICANT: Michiels, Frank
; APPLICANT: Morioka, Sinji
; APPLICANT: Scheirlinck, Trees
; APPLICANT: Komari, Toshihiko
; TITLE OF INVENTION: Stamen-specific Promoters from Rice
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5639948west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,072B
; FILING DATE: 05-AUG-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 9200272
; FILING DATE: 06-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91403352.7
; FILING DATE: 10-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91402590.3
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91400318.1
; FILING DATE: 08-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 8076.93USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: rice
; TISSUE TYPE: anther
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..322
; OTHER INFORMATION: /product= "cDNA T23"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 333..347
; OTHER INFORMATION: /product= "cloning adaptor
; OTHER INFORMATION: sequence"
US-08-104-072B-2

Query Match 3.5%; Score 46; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1281 TGTAAAAA 1326
Db 284 TGTAAAAA 329

RESULT 7

US-09-461-325-28
; Sequence 28, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-325-28

Query Match 3.5%; Score 46; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
Db 470 TGTAAAAA 515

RESULT 8

US-09-385-982-262/c
; Sequence 262, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGS, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-08-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 262
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(593)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-262

Query Match 3.5%; Score 46; DB 3; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
Db 75 TGTAAAAA 30

RESULT 9

US-09-461-325-129
; Sequence 129, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 129
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-325-129

Query Match 3.5%; Score 46; DB 4; Length 1660;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
Db 1615 TGTAAAAA 1660

RESULT 10

US-09-801-052-1
; Sequence 1, Application US/09801052
; Patent No. 6368642
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001045
; CURRENT APPLICATION NUMBER: US/09/801,052
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1872
; TYPE: DNA

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; ORGANISM: Human
US-09-801-052-1

Query Match      3.5%; Score 46; DB 4; Length 1872;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
Db 1765 TGTAAAAA 1810

RESULT 11
US-09-819-993-1
; Sequence 1, Application US/09819993
; Patent No. 6436692
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; FILE REFERENCE: CLO01195
; CURRENT APPLICATION NUMBER: US/09/819,993
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2002
; TYPE: DNA
; ORGANISM: Human
US-09-819-993-1

Query Match      3.5%; Score 46; DB 4; Length 2002;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
Db 1956 TGTAAAAA 2001

RESULT 12
US-09-996-243-302
; Sequence 302, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumás, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C13
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; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
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; PRIOR FILING DATE: 1998-06-19
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; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/090472
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Db 2061 TGTAAA 2106

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US-09-149-476-163
; Sequence 163, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002PI
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,617

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; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1281 TGTAAA 1326
Db 2144 TGTAAA 2189

RESULT 14

US-09-569-804-20
; Sequence 20, Application US/09569804
; Patent No. 6506962

; GENERAL INFORMATION:

; APPLICANT: Bougri, Oleg
; APPLICANT: Rommens, Cains
; APPLICANT: Srivastava, Neelam
; APPLICANT: Swords, Kathleen M
; TITLE OF INVENTION: Acquired Resistance Genes in Plants
; FILE REFERENCE: 38-21(15415)

; CURRENT APPLICATION NUMBER: US/09/569,804

; CURRENT FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: 60/133,965

; PRIOR FILING DATE: 1999-05-13

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 2235

; TYPE: DNA

; ORGANISM: Zea mays

US-09-569-804-20

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RESULT 15

US-09-245-041-18

; Sequence 18, Application US/09245041

; Patent No. 6274339

; GENERAL INFORMATION:

; APPLICANT: Moore, K.

; APPLICANT: Nagle, D.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; FILE REFERENCE: 7853-136

; CURRENT APPLICATION NUMBER: US/09/245,041

; CURRENT FILING DATE: 1999-02-05

; EARLIER APPLICATION NUMBER: 60/093,630

; EARLIER FILING DATE: 1998-07-21

; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 18

; LENGTH: 2625

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-245-041-18

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Qy 1281 TGTAAA 1326
Db 2574 TGTAAA 2619

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Job time : 108 secs

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 18:41:31 ; Search time 443 Seconds
(without alignments)
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Searched: 2141354 seqs, 159547879 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	48	3.6	1522	9	US-09-805-550-1
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4	47	3.5	112	10	US-09-768-837-51
5	47	3.5	939	13	US-10-078-929-89
6	47	3.5	1015	11	US-09-984-245-111
7	47	3.5	1015	11	US-09-966-262-111
8	47	3.5	1015	11	US-09-983-966-111
9	47	3.5	1015	14	US-10-143-080-111
10	47	3.5	1201	14	US-10-012-542-36
11	47	3.5	1371	9	US-03-764-853-227
12	47	3.5	2968	9	US-09-925-301-584
13	47	3.5	2976	14	US-10-106-698-1500
14	47	3.5	2976	14	US-10-027-000-1
15	46	3.5	269	14	US-10-102-524-963
16	46	3.5	292	10	US-09-960-352-12176

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Sequence 28, Appl	530	3.5	14	US-10-012-842-28
Sequence 9, Appl	589	3.5	12	US-10-417-510-9
Sequence 262, App	593	3.5	11	US-09-871-161-262
Sequence 41, Appl	773	3.5	9	US-09-764-898-41
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Sequence 392, Appl	773	3.5	9	US-09-764-877-992
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;; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
;; FILE REFERENCE: BS1357 US NA

;; CURRENT APPLICATION NUMBER: US/10/078,929

;; CURRENT FILING DATE: 2002-02-19

;; PRIOR APPLICATION NUMBER: 09/566,394

;; PRIOR FILING DATE: 2000-05-05

;; PRIOR APPLICATION NUMBER: 60/133038

;; PRIOR FILING DATE: 1999-05-07

;; PRIOR APPLICATION NUMBER: 60/133042

;; PRIOR FILING DATE: 1999-05-07

;; PRIOR APPLICATION NUMBER: 60/133427

;; PRIOR FILING DATE: 1999-05-11

;; PRIOR APPLICATION NUMBER: 60/133437

;; PRIOR FILING DATE: 1999-05-11

;; PRIOR APPLICATION NUMBER: 60/133428

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;; PRIOR FILING DATE: 1999-05-11

;; PRIOR APPLICATION NUMBER: 60/133436

;; PRIOR FILING DATE: 1999-05-11

;; PRIOR APPLICATION NUMBER: 60/137667

;; PRIOR FILING DATE: 1999-06-04

;; NUMBER OF SEQ ID NOS: 208

;; SOFTWARE: Microsoft Office 97

;; SEQ ID NO 89

;; LENGTH: 939

;; TYPE: DNA

;; ORGANISM: Glycine max

;; US-10-078-929-89

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QY 1280 GTGTAAAAA 1326

DB 886 GTGTAAAAA 932

RESULT 6

US-09-984-245-111

;; Sequence 111, Application US/09984245

;; Patent No. US20020165374A1

;; GENERAL INFORMATION:

;; APPLICANT: Young et al.

;; TITLE OF INVENTION: 87 Human Secreted Proteins

;; FILE REFERENCE: P2004P1

;; CURRENT APPLICATION NUMBER: US/09/984,245

;; CURRENT FILING DATE: 2001-10-29

;; PRIOR APPLICATION NUMBER: 09/154,707

;; PRIOR FILING DATE: 1998-09-17

;; PRIOR APPLICATION NUMBER: PCT/US98/05311

;; PRIOR FILING DATE: 1998-03-19

;; PRIOR APPLICATION NUMBER: US 60/041,277

;; PRIOR FILING DATE: 1997-03-21

;; PRIOR APPLICATION NUMBER: US 60/042,344

;; PRIOR FILING DATE: 1997-03-21

;; PRIOR APPLICATION NUMBER: US 60/041,276

;; PRIOR FILING DATE: 1997-03-21

;; PRIOR APPLICATION NUMBER: US 60/041,281

;; PRIOR FILING DATE: 1997-03-21

;; PRIOR APPLICATION NUMBER: US 60/048,094

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,350

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,188

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,135

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/050,937

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;; PRIOR APPLICATION NUMBER: US 60/048,187

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;; PRIOR APPLICATION NUMBER: US 60/048,352

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,186

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,069

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,095

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,131

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,096

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,355

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,160

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,351

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,154

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/054,804

;; PRIOR FILING DATE: 1997-08-05

;; PRIOR APPLICATION NUMBER: US 60/056,370

;; PRIOR FILING DATE: 1997-08-19

;; PRIOR APPLICATION NUMBER: US 60/060,862

;; PRIOR FILING DATE: 1997-10-02

;; NUMBER OF SEQ ID NOS: 343

;; SOFTWARE: Patentin ver. 2.0

;; SEQ ID NO 111

;; LENGTH: 1015

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; NAME/KEY: misc feature

;; LOCATION: (1013)

;; OTHER INFORMATION: n equals a,t,g, or c

;; US-09-984-245-111

Query Match 3.5%; Score 47; DB 10; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 947 GTGTAAAAA 993

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US-09-966-262-111

;; Sequence 111, Application US/09966262

;; Publication No. US20030050461A1

;; GENERAL INFORMATION:

;; APPLICANT: Young et al.

;; TITLE OF INVENTION: 87 Human Secreted Proteins

;; FILE REFERENCE: P2004P1

;; CURRENT APPLICATION NUMBER: US/09/966,262

;; CURRENT FILING DATE: 2001-10-01

;; PRIOR APPLICATION NUMBER: US 09/154,707

;; PRIOR FILING DATE: 1998-09-17

;; PRIOR APPLICATION NUMBER: PCT/US98/05311

;; PRIOR FILING DATE: 1998-03-19

;; PRIOR APPLICATION NUMBER: US 60/041,277

;; PRIOR FILING DATE: 1997-03-21

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;; PRIOR APPLICATION NUMBER: US 60/041,276

;; PRIOR FILING DATE: 1997-03-21

;; PRIOR APPLICATION NUMBER: US 60/041,281

;; PRIOR FILING DATE: 1997-03-21

;; PRIOR APPLICATION NUMBER: US 60/048,094

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; PRIOR APPLICATION NUMBER: US 60/048,350
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; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 1015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1014)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-966-262-111

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Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1326
DB 947 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 993

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; Publication No. US20030060619A1
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; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
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; PRIOR APPLICATION NUMBER: US 60/041,277
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; PRIOR FILING DATE: 1997-03-21
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; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
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; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
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; SEQ ID NO 111
; LENGTH: 1015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1014)
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US-09-983-966-111

Query Match          3.5%; Score 47; DB 11; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
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DB 947 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 993

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; Sequence 111, Application US/10143090
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; Publication No. US20030109690A1
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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA00581
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1500
; LENGTH: 2968
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: misc feature
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US-10-106-698-1500

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Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20030119006A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Goedegebuur, Frits
; APPLICANT: Ward, Michael
; APPLICANT: Yao, Jian
; TITLE OF INVENTION: BGL4 Beta-Glucosidase and Nucleic Acids
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: GC696
; CURRENT APPLICATION NUMBER: US/10/027,000
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Trichoderma reesei
US-10-027-000-1

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Best Local Similarity 100.0%; Pred. No. 3.2e-12;
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RESULT 15
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; Sequence 963, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 963
; LENGTH: 269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-524-963

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Best Local Similarity 100.0%; Pred. No. 9.6e-12;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1281 TGTAAAAA 1326
Db 158 TGTAAAAA 203

Search completed: November 7, 2003, 21:02:16
Job time : 465 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 16:57:25 ; Search time 3088 Seconds
(without alignments)
10436.443 Million cell updates/sec

Title: US-10-024-806-1

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Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

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Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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6: em_estpl:*

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8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

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17: em_gss_hum:*

18: em_gss_inv:*

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	9	457	34.5	457	14	CD510389
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	144	47	3.5	330	9	AI812107	AI812107 tw77d02.x	217	47	3.5	585	12	BI384363
	145	47	3.5	331	14	CB722623	CB722623 UT-M-GHO-	218	47	3.5	588	14	CD417119
	146	47	3.5	333	14	CA779308	CA779308 MEL384_8	219	47	3.5	626	14	CD396229
	147	47	3.5	337	13	B0529438	B0529438 AGENCOURT	220	47	3.5	632	12	BI896262
	148	47	3.5	338	9	AV692389	AV692389 AV692389	221	47	3.5	633	12	BI896262
	149	47	3.5	340	10	BE804624	BE804624 st-84c12.y	222	47	3.5	639	13	BQ197444
	150	47	3.5	340	13	BQ636085	BQ636085 hd04c02.y	223	47	3.5	644	14	CD400785

370	46	3.5	167	14	CB449421	CB449421 703619 MA	443	197	10	BF595660	BF595660 su78h10.Y
C 371	46	3.5	168	14	CA342847	CA342847 672803 NC	444	197	14	CB947040	CB947040 AGENCOURT
372	46	3.5	169	9	AA267695	AA267695 mz66a03.x	C 445	197	14	CB978492	CB978492 CAB48005
373	46	3.5	169	9	BE891834	BE891834 601434280	446	197	14	CD422811	CD422811 laa82c05-
374	46	3.5	169	12	BJ332062	BJ332062 BJ332062	447	198	9	AA689795	AA689795 vt61e03.x
375	46	3.5	173	12	BI145661	BI145661 602909801	448	198	12	BI782550	BI782550 kn27c04.Y
376	46	3.5	173	12	BI738659	BI738659 603358879	449	198	13	BU096447	BU096447 tca-932 t
377	46	3.5	173	14	CA819116	CA819116 sau69c08.	450	199	10	BF754990	BF754990 QVO-CT058
378	46	3.5	174	14	CB409269	CB409269 NISC.nc04	451	199	10	BE807222	BE807222 ss13e02.Y
C 379	46	3.5	176	9	AA590383	AA590383 vn58h08.x	452	199	10	BM896894	BM896894 ph49d05.Y
380	46	3.5	176	14	CD401642	CD401642 Gm.k2402	453	200	12	BQ288161	BQ288161 DJ54d08.Y
381	46	3.5	177	9	AL039137	AL039137 DXFZP566L	454	200	13	BU565550	BU565550 AGENCOURT
382	46	3.5	178	10	BG164558	BG164558 602342109	455	200	14	CD522046	CD522046 AGENCOURT
383	46	3.5	178	10	BG285326	BG285326 602409573	456	201	9	AW186498	AW186498 ses8f01.Y
C 384	46	3.5	178	14	CA608901	CA608901 wr1.pk009	457	201	9	AW756874	AW756874 sk82c06.Y
385	46	3.5	180	9	AL714827	AL714827 AL714827	458	202	12	BM896762	BM896762 ph47f01.Y
386	46	3.5	180	9	AW036957	AW036957 614022H05	459	203	12	BM307805	BM307805 sak34c04.
387	46	3.5	180	12	BM030226	BM030226 488800 MA	460	203	9	AJ227642	AJ227642 C1C26R C1
388	46	3.5	181	14	CA342725	CA342725 672670 NC	461	205	9	AL837271	AL837271 AL837271
389	46	3.5	182	12	BI941588	BI941588 sc74f10.Y	462	206	9	AA212981	AA212981 mw85c01.x
390	46	3.5	182	12	BI945726	BI945726 sc66a04.Y	463	206	13	BQ564936	BQ564936 g127f10.Y
391	46	3.5	182	14	CB059684	CB059684 4009825 B	464	206	14	CD353930	CD353930 UT-M-GM0-
C 392	46	3.5	183	9	AL696076	AL696076 DXFZP686A	465	207	10	BE024105	BE024105 sm96c06.Y
393	46	3.5	184	9	AJ652664	AJ652664 wb30d02.x	466	207	13	BQ611375	BQ611375 sap5sa12.
394	46	3.5	184	9	AJ437747	AJ437747 AJ437747	C 467	208	9	AL501524	AL501524 AU501524
395	46	3.5	184	9	AW656560	AW656560 108879 MA	468	208	9	AW099490	AW099490 sd41e01.Y
396	46	3.5	184	10	BF340889	BF340889 602037794	469	208	9	AW311554	AW311554 sg41e02.Y
397	46	3.5	184	12	BM309415	BM309415 sak58d01.	470	208	10	BG155209	BG155209 sab41d03.
398	46	3.5	184	14	CA819494	CA819494 sau79d07.	C 471	208	12	BG991160	BG991160 NX2V-HT118
399	46	3.5	185	12	BG981746	BG981746 MR3-CN014	472	208	12	BM158603	BM158603 MYLV 036
400	46	3.5	185	12	BI714719	BI714719 ic04h09.Y	473	209	14	CA807128	CA807128 ESG016b.E
401	46	3.5	185	13	BQ129803	BQ129803 i131b09.Y	474	209	14	CA807128	CA807128 ESG016b.E
402	46	3.5	185	14	CB951603	CB951603 AGENCOURT	C 475	210	13	BQ800159	BQ800159 EST 7194
403	46	3.5	186	9	AW317352	AW317352 sg48b11.Y	476	211	12	BI746984	BI746984 tm34d11.Y
404	46	3.5	186	10	BG382271	BG382271 298031 MA	477	211	13	BQ799392	BQ799392 RST 1561
405	46	3.5	186	12	BI941959	BI941959 se15d06.Y	C 478	211	13	BQ799392	BQ799392 RST 1561
406	46	3.5	186	13	BU531778	BU531778 AGENCOURT	479	211	13	BQ799392	BQ799392 RST 1561
407	46	3.5	186	13	BU944985	BU944985 AGENCOURT	480	212	14	CB060012	CB060012 4010019 B
408	46	3.5	187	10	BF970768	BF970768 602273782	481	213	12	BI345522	BI345522 374374 MA
409	46	3.5	187	11	CNS09K7K	CNS09K7K Single re	482	213	12	BI345522	BI345522 374374 MA
410	46	3.5	187	14	CA337036	CA337036 NISC.lv08	483	214	9	AA217651	AA217651 mu98c02.Y
411	46	3.5	188	9	AW031158	AW031158 AU031158	484	214	9	AW099547	AW099547 sd43c07.Y
412	46	3.5	189	9	AL707832	AL707832 DXFZP686L	485	214	9	AW065534	AW065534 s157g03.Y
413	46	3.5	189	10	BF527014	BF527014 602070296	486	214	13	EX476103	EX476103 DXFZP686F
414	46	3.5	189	12	BI652330	BI652330 603299790	487	214	14	C90990	C90990 C90990 Dict
C 415	46	3.5	190	10	BG631028	BG631028 cc-esf1cL	488	214	14	CA819119	CA819119 sau69d04.
416	46	3.5	190	12	BG956196	BG956196 QV1-CT075	489	214	14	CA935250	CA935250 sau51b02.
417	46	3.5	190	12	BM025324	BM025324 fs77a04.Y	490	215	9	AL716626	AL716626 sau51b02.
C 418	46	3.5	190	14	CB410004	CB410004 NISC.nc08	491	215	13	BQ802041	BQ802041 WHE2821.D
419	46	3.5	191	9	AA637077	AA637077 vt07h01.x	C 492	216	12	BM889168	BM889168 KD06f01.Y
C 420	46	3.5	191	9	AA654391	AA654391 nt03e02.s	493	216	13	BQ799325	BQ799325 EST 1494
421	46	3.5	191	9	AW099546	AW099546 sd43c06.Y	494	216	13	BU521241	BU521241 AGENCOURT
422	46	3.5	191	10	BG058150	BG058150 nah21c09.	495	216	14	CA818865	CA818865 sau65c03.
423	46	3.5	191	10	BF299883	BF299883 602030521	496	216	14	CA819253	CA819253 sau71e04.
424	46	3.5	191	12	BI671447	BI671447 fs48d10.Y	497	217	12	BE023962	BE023962 sm94g03.Y
425	46	3.5	191	12	BJ334254	BJ334254 BJ334254	C 498	217	12	BM493457	BM493457 NLXV 064
426	46	3.5	192	9	AW344858	AW344858 26344 MAR	499	218	9	AI628337	AI628337 ts63g06.x
427	46	3.5	192	9	AA388573	AA388573 vc95h05.x	500	218	9	AA396449	AA396449 vb27e07.Y
428	46	3.5	192	12	BI539237	BI539237 451488 MA	C 501	219	9	AI619662	AI619662 ty51d12.x
429	46	3.5	192	12	BJ330858	BJ330858 BJ330858	502	219	9	AW268122	AW268122 x5-92h07.x
C 430	46	3.5	193	9	AW089387	AW089387 xd04h06.x	503	219	9	AA596321	AA596321 v026d10.x
431	46	3.5	193	12	BM271421	BM271421 sak09c02.	504	219	10	BE978474	BE978474 ds80c01.Y
432	46	3.5	194	9	AW184786	AW184786 se82d11.Y	505	219	12	BM307274	BM307274 sak27a02.
433	46	3.5	194	9	AW734665	AW734665 sk97h03.Y	C 506	219	14	CA757467	CA757467 BR0500110
434	46	3.5	194	12	BI782405	BI782405 kh25c03.Y	507	220	9	AA267483	AA267483 mw72g05.x
435	46	3.5	194	12	BM092222	BM092222 eah09g02.	508	220	10	BG237383	BG237383 sab06b07.
436	46	3.5	194	12	BM093888	BM093888 sah22d10.	509	221	12	BG950514	BG950514 PM0-CT070
437	46	3.5	194	14	CD857623	CD857623 NISC.na08	510	221	13	BX248924	BX248924 BX248924
438	46	3.5	194	14	CD387849	CD387849 AGENCOURT	511	222	12	BI909914	BI909914 603070551
C 439	46	3.5	195	12	BG983776	BG983776 MR4-CN014	512	222	13	AI805642	AI805642 tx97f09.x
440	46	3.5	195	12	BG991086	BG991086 MR2-HT118	C 513	223	10	BG250190	BG250190 602362306
441	46	3.5	196	10	BE758591	BE758591 SC0100 Th	514	223	12	BM898153	BM898153 ph60d11.Y
442	46	3.5	197	9	AW133441	AW133441 se19a07.Y	C 515	223	14	CB410539	CB410539 NISC.nc12

C 516 46 3.5 224 9 AI582910 ts07e04.x 589 46 3.5 250 9 AU262843
517 46 3.5 224 9 AI609967 tt78b07.x 590 46 3.5 250 14 CA715111
518 46 3.5 224 12 BI699064 sg93c06. 591 46 3.5 252 9 AU263302
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523 46 3.5 228 9 AU097528 AU097528 596 46 3.5 253 9 AA596935
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532 46 3.5 231 9 AA250449 AA250449 mz59d06.x 605 46 3.5 258 14 CB944780
533 46 3.5 231 10 BF348723 BF348723 JAYS0013. 606 46 3.5 259 12 BM983229
534 46 3.5 231 10 BE749895 BE749895 200970 MA 607 46 3.5 259 13 BQ107860
535 46 3.5 231 13 BU851863 BU851863 AGENCOURT 608 46 3.5 261 13 BX476487
536 46 3.5 232 9 AW081349 AW081349 xc41b07.x 609 46 3.5 262 9 AI590918
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539 46 3.5 233 10 BG452647 BG452647 NF079B01L 612 46 3.5 263 12 BM966779
540 46 3.5 233 12 BI423831 BI423831 saf18e05. 613 46 3.5 263 12 BI396482
541 46 3.5 234 9 AU094659 AU094659 614 46 3.5 264 12 BM495162
542 46 3.5 234 10 BE807978 BE807978 213073 MA 615 46 3.5 265 10 BF753027
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587 46 3.5 249 12 BM055889 BM055889 1d84c02.Y 660 46 3.5 282 9 AA596374
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C 808	46	3.5	340	12	BM569511	BM569511 kJ62f10.Y	881	367	9	AL643167	AL643167
C 809	46	3.5	340	13	BM798704	BM798704 EST 1873	882	367	14	CB000271	CB000271 S345T.G06
C 810	46	3.5	340	13	BM851144	BM851144 AGNCOURT	883	368	13	BY673667	BY673667
C 811	46	3.5	340	14	CD351386	CD351386 UI-M-GIO-	884	368	14	CD392542	CD392542 Gm ck1173
C 812	46	3.5	341	13	BM762496	BM762496 sap28b05.	885	369	9	AA423575	AA423575 ve7605.r
C 813	46	3.5	341	14	CB079723	CB079723 hp75f04.b	886	369	10	BE235634	BE235634 143193.MA
C 814	46	3.5	342	14	CA802780	CA802780 sau42a09.	887	369	12	BM569755	BM569755 1n97b02.Y
C 815	46	3.5	342	9	AI362522	AI362522 qv72d07.x	888	370	10	BE684533	BE684533 186001.MA
C 816	46	3.5	343	10	BM043626	BM043626 sv39b03.Y	889	370	9	AV760402	AV760402
C 817	46	3.5	343	14	CA337467	CA337467 NISC_lw01	890	371	9	AW335588	AW335588 S49B4.AGS
C 818	46	3.5	343	14	CA339882	CA339882 ELQ1N0310	891	371	9	AA390241	AA390241 CPST.231
C 819	46	3.5	343	14	CB693218	CB693218 AGNCNUT:N	892	371	10	BM632517	BM632517 GMD9846.5
C 820	46	3.5	344	9	AA033195	AA033195 mi39h01.r	893	371	14	CB075829	CB075829 h251h02.b
C 821	46	3.5	344	9	AA611786	AA611786 v05b06.r	894	372	9	AA804302	AA804302 nw31h11.s
C 822	46	3.5	344	14	CB084212	CB084212 hqlf111.b	895	372	14	CB075829	CB075829
C 823	46	3.5	345	9	AA616335	AA616335 vn65a10.r	896	373	10	BM382618	BM382618
C 824	46	3.5	345	14	CB705871	CB705871 AGNCNUT:U	897	373	12	BI376731	BI376731 BFLG3.000
C 825	46	3.5	346	12	BM207280	BM207280 BM707280	898	373	12	BM495109	BM495109 JPCGB1.4
C 826	46	3.5	347	14	CB523220	CB523220 UI-M-GK0-	899	373	14	CA486557	CA486557 WHE4333.B
C 827	46	3.5	348	9	AA038807	AA038807 mi95b04.r	900	373	14	CA819740	CA819740 sau75d01.
C 828	46	3.5	348	9	AL644569	AL644569 AL644569	901	374	9	AV712612	AV712612
C 829	46	3.5	348	9	AA085983	AA085983 AU085983	902	374	14	CA668301	CA668301 w1sul.pk0
C 830	46	3.5	348	10	BM383179	BM383179 301132.MA	903	374	14	CB094952	CB094952 h277c02.b
C 831	46	3.5	349	12	BI378856	BI378856 BFLG1.000	904	375	12	BI704162	BI704162 x063g04.Y
C 832	46	3.5	349	14	CA302118	CA302118 taal0601.	905	375	14	CB830500	CB830500 r117r03.Y
C 833	46	3.5	349	14	CA764732	CA764732 AP53.Pdf	906	377	10	BM389157	BM389157
C 834	46	3.5	350	12	BM905276	BM905276 AGNCOURT	907	377	12	BM525528	BM525528
C 835	46	3.5	350	13	EQ398164	EQ398164 NISC.mo05	908	377	13	BY669070	BY669070
C 836	46	3.5	351	14	CB781081	CB781081 AGNCNUT:S	909	379	9	AL047570	AL047570
C 837	46	3.5	351	9	AW485985	AW485985 69165.NAR	910	379	13	BQ394195	BQ394195 NISC.RG07
C 838	46	3.5	352	9	AI292655	AI292655 GH15605.5	911	379	14	C99698	C99698 C99698.Rice
C 839	46	3.5	352	13	BY392467	BY392467 BX192467	912	380	9	AV076356	AV076356 AU076356
C 840	46	3.5	353	9	AA218987	AA218987 zrl1905.s	913	380	12	EG994653	EG994653 355348.MA
C 841	46	3.5	353	9	AW192300	AW192300 x184a11.x	914	381	14	BY669201	BY669201
C 842	46	3.5	354	9	AW738898	AW738898 vv62c12.r	915	381	14	C99068	C99068 C99068.Rice
C 843	46	3.5	354	12	BM886657	BM886657 sam19e02.	916	381	14	CB809622	CB809622 AGNCNUT:S
C 844	46	3.5	354	13	BQ453941	BQ453941 sap02e03.	917	382	12	BM63366	BM63366 AU63366
C 845	46	3.5	354	13	BQ623840	BQ623840 USDA-PP.0	918	383	12	BM889208	BM889208 R507b10.Y
C 846	46	3.5	355	9	AW832430	AW832430 sm10c09.Y	919	383	13	BY465286	BY465286 BY465286
C 847	46	3.5	355	13	BQ078177	BQ078177 fY85d08.Y	920	384	10	BE629296	BE629296 uu36c07.Y
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C 849	46	3.5	355	13	BQ634559	BQ634559 NRRV070.D	922	384	14	CB094493	CB094493 h270f09.D
C 850	46	3.5	355	14	CD415635	CD415635 Gm ck5345	923	384	14	CD414752	CD414752 Gm ck4753
C 851	46	3.5	356	9	AI976772	AI976772 ESN271366	924	385	9	AV975649	AV975649 AV975649
C 852	46	3.5	356	9	AW569308	AW569308 sl76d07.Y	925	385	12	BI377795	BI377795 BFLG3.001
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C 854	46	3.5	358	9	AW560287	AW560287 AJ560287	927	386	13	BQ220002	BQ220002 AGNCOURT
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C 856	46	3.5	358	13	BQ287097	BQ287097 i162c11.Y	929	387	9	AI457343	AI457343 t173b03.X
C 857	46	3.5	358	14	CB018582	CB018582 PX49C02.Y	930	388	10	BE055033	BE055033 GA_Ea001
C 858	46	3.5	359	12	BI906993	BI906993 603064939	931	388	12	BM155487	BM155487 fW06G08.Y
C 859	46	3.5	359	13	BQ155641	BQ155641 NF08F011	932	388	14	CA935003	CA935003 sau62e02.
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C 865	46	3.5	361	9	AW174992	AW174992 AU174992	938	391	13	BUS41473	BUS41473 AGNCOURT
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C 867	46	3.5	362	9	AW706525	AW706525 sj57f06.Y	940	392	9	AW820605	AW820605 AL820605
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C 874	46	3.5	364	14	CA348393	CA348393 679694.NC	947	393	10	EG112028	EG112028 602281873
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C 879	46	3.5	365	12	BM285328	BM285328 pb12e03.Y	952	395	10	BF815855	BF815855 WR2-C1012
C 880	46	3.5	366	10	BE419061	BE419061 WWR018.E6	953	395	12	BI381051	BI381051 BFLG1_002

954	396	9	AU263111	AU263111	JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
955	397	9	AW058913	fes0e09.x	COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
956	397	10	AW989051	ug12e08.Y	FEATURES	Location/Qualifiers
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963	398	13	BU774392	SJRGKE04	/notes="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"	
964	399	9	A1118304	ue39h02.x	BASE COUNT	361 a 315 c 343 g 323 t
965	399	9	AA396149	vb44f06.x	ORIGIN	
966	399	10	AA9113035	uf48c04.Y	Query Match	100.0%; Score 1326; DB 11; Length 1342;
967	399	14	CB700255	AMGNWOC:N	Best Local Similarity	100.0%; Pred. No. 7,8e-175;
968	400	9	AU060236	sh32b03.Y	Matches 1326; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
969	400	9	AW596423	sj12c04.Y	QY	1 GCGGGAGCTTCCAAAGCCCGCTCCCAATAGACTCTCCCATCGTCTCTGCTCC 60
970	400	13	BQ795601	EST 4539	Db	17 GCGGGAGCTTCCAAAGCCCGCTCCCAATAGACTCTCCCATCGTCTCTGCTCC 76
971	400	13	BQ795601	EST 4539	QY	61 GTACCGGCTCAATPACTCCGCTGCATCTCCAAAGACACTGCTCCCTCTGGCTCCGC 120
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973	400	14	CB089323	qs07g07.b	QY	121 CTCTCTTGGCTCTTGGGTCCTCCGAGCGCCCTCATGCGCCAGCGCGCGCCGACCGCA 180
974	402	9	A1356505	qz22b04.x	Db	137 CTCTCTTGGCTCTTGGGTCCTCCGAGCGCCCTCATGCGCCAGCGCGCGCCGACCGCA 196
975	402	9	AU095196	AU095196	QY	181 GCACGACGACGACTCTCTCCCGGCTCGGCTGAGCAGCGCGCGCGCGCGCTCC 240
976	402	10	BF793137	602254140	Db	197 GCACGACGACGACTCTCTCCCGGCTCGGCTGAGCAGCGCGCGCGCGCTCC 256
977	402	14	CA803718	ESG0110b.	QY	241 GCGCGGGGTTGCTGACGTTTGGTGGAGGCGCGCGCTTCTCTCCACGCTCGGCTCC 300
978	403	9	AA831733	oc93a04.S	Db	257 GCGCGGGGTTGCTGACGTTTGGTGGAGGCGCGCGCTTCTCTCCACGCTCGGCTCC 316
979	403	13	BQ801653	WHE2817.A	QY	301 GCGCGTGGGTTCTCTGGTGTGCAAAACCGATGTTGCTGTTACAGTGATCTAGAGGATTTGGT 420
980	404	9	AW066606	683003H03	Db	317 GCGCGTGGGTTCTCTGGTGTGCAAAACCGATGTTGCTGTTACAGTGATCTAGAGGATTTGGT 436
981	404	12	BI494234	BI494234	QY	361 GATCTCAAGCTGGAAGCTCCAGTGTGTTGTTTACAGTGATCTAGAGGATTTGGT 480
982	404	12	BI902057	id17b12.Y	Db	377 GATCTCAAGCTGGAAGCTCCAGTGTGTTGTTTACAGTGATCTAGAGGATTTGGT 496
983	404	12	BM922557	AGENCOURT	QY	421 AAGCAACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGGTTCTGTGTAACATATGCCCGG 540
984	404	13	BY392337	BY392337	Db	437 AAGCAACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGGTTCTGTGTAACATATGCCCGG 556
985	404	9	AU033042	AU033042	QY	481 TCCTCGAAAGGGCTGGAAGGCTCCAAAGAGATTGAAGATCTGGTGTGAGGCTATTC 600
986	405	14	CA813308	sa072d07.	Db	541 ACCTTTCCGAGGAGATGTTTCAAAGAGAGCTGATCTAGAGTCTATGATCAAGAGCTCTTA 616
987	406	13	BU188267	AGENCOURT	QY	557 ACCTTTCCGAGGAGATGTTTCAAAGAGAGCTGATCTAGAGTCTATGATCAAGAGCTCTTA 660
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989	406	13	BU925902	sa83f04.		
990	406	9	AA810605	ob64c09.s		
991	407	9	AL718978	AL718978		
992	408	12	EM077515	pb18d01.Y		
993	408	14	CB453559	709434.MA		
994	409	12	BI697681	60334862		
995	410	9	AJ433799	AJ433799		
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997	410	12	EM333331	MEST189-C		
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ALIGNMENTS

RESULT 1	AY106146	1342 bp	linear	HTC 16-OCT-2002
LOCUS	AY106146			
DEFINITION	Zea mays PCO074795 mRNA sequence.			
ACCESSION	AY106146			
VERSION	AY106146.1	GI:21209224		
KEYWORDS	HTC.			
SOURCE	Zea mays			
ORGANISM	Zea mays			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogoneae; Zea.			
AUTHORS	1 (bases 1 to 1342)			
TITLE	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.			
JOURNAL	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes			
REFERENCE	Unpublished (2002)			
AUTHORS	2 (bases 1 to 1342)			
TITLE	Coe, E.H.			
	Direct Submission			

QY 661 TTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAAATGATCTGAATCTTACTGGCGTC 720
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 QY 677 TTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAAATGATCTGAATCTTACTGGCGTC 736
 Db |||||
 QY 721 TTCCTTTGTACACAGGCTGCAACAAAGATATGATGAAAGAGAGAAAGGGGAAAAATATC 780
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 QY 737 TTCCTTTGTACACAGGCTGCAACAAAGATATGATGAAAGAGAGAAAGGGGAAAAATATC 796
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 QY 781 AACATTCACATCTAGTGGTCTTACTGGCAATCTTGGCCAGCTAATATATAGCGCAGCC 840
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 QY 857 AAGCTGGAGTGAATGGTTTACAAAAACAGTCCAGGAGATGCAAGCAGAGAAATATC 916
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 QY 1321 AAAAAA 1326
 Db |||||
 QY 1337 AAAAAA 1342
 Db |||||

RESULT 2
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 LOCUS
 DEFINITION 646 bp mRNA linear EST 16-MAY-2003
 3529_1_61_1_C02.Y.1 3529 - 2 mm ear tissue from Schmidt and Hake
 labs Zea mays cDNA, mRNA sequence.
 ACCESSION CB604782
 VERSION CB604782.1
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 646)
 Walbot,V.
 Zea mays
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished
 CONTACT Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 3529_1_61_1 row: C column: 02.
 Location/Qualifiers
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 /clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake
 labs"
 /notes="Organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoRI;
 Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu
 amplified. Ampicillin is the selection marker."
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Query Match 46.8%; Score 620; DB 14; Length 646;
 Best Local Similarity 100.0%; Pred. No. 2.5e-77;
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 QY 87 GGCTTCCCGCTCTCTTCCGCTTCCGCTCCCGAGCCCTCATGSCCAGCCGCCG 146
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 QY 567 AGCAGCTCTAGATAAATGGGAGCAATAGATGCTGTTGTTAAATTAATGCAAGGATTACG 626
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RESULT 3
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 DEFINITION 1091024E01.y3 1091 - Immature ear with common ESTs screened by
 BQ293972 600 bp mRNA linear EST 15-MAY-2002

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Schmidt lab Zea mays cDNA, mRNA sequence.
B0293972.1 GI:20802922
VERSION B0293972.1
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE clade; Panicoideae; Andropogoneae; Zea.
JOURNAL Walbot, V.
COMMENT Zea mays
Maize ESTs from various cDNA libraries sequenced at Stanford
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1091024 row: E column: 01.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.4e-68;
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 22 GTCTTCTTTGTACACAGGCTGCACAAAGTAATGTAAGAAAGAGAAAGGGAATTT 81
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Db 142 GCCAAGCTGAGTGATGTTTTCACAAAACAGTTCGCCAGGGAGTATGCAAGCAGAAAT 201
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Db 322 GAATTCAGGGTTGGTGGAGTTCCTGGCCCTTAACCCCGCAGCTAGCTATATGACTGGA 381
QY 1078 CAGTGTCTTCAATGACGGGGGATGTAATGTAAGATTGAGTTGACTTGTATGCACTT 1137
Db 382 CAGTGTCTTCAATGACGGGGGATGTAATGTAAGATTGAGTTGACTTGTATGCACTT 441
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BU092521
LOCUS 946152D04.y1 946 - tassell primordium prepared by Schmidt lab Zea
DEFINITION mays cDNA, mRNA sequence.
ACCESSION BU092521
VERSION BU092521.1 GI:22542083
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE clade; Panicoideae; Andropogoneae; Zea.
JOURNAL Walbot, V.
COMMENT Zea mays
Maize ESTs from various cDNA libraries sequenced at Stanford
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946152 row: D column: 04.
Location/Qualifiers
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inflorescence development"
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/clone_lib="946 - tassell primordium prepared by Schmidt
lab"
/notes="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI;
Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybridZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."
BASE COUNT 168 a 96 c 137 g 156 t
ORIGIN
Query Match 41.5%; Score 550; DB 13; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.2e-67;
Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 719 TCTTCTTTGTACACAGGCTGCACAAAGTAATGTAAGAAAGAGAAAGGGAATTTA 778
Db 1 TCTTCTTTGTACACAGGCTGCACAAAGTAATGTAAGAAAGAGAAAGGGAATTTA 60
QY 779 TCAACATTCATCTGTAGTTGGTCTTACTGGCAATGTTGCCCAAGCTAATTATAGCGCAG 838
Db 61 TCAACATTCATCTGTAGTTGGTCTTACTGGCAATGTTGCCCAAGCTAATTATAGCGCAG 120
QY 839 CCAAGGCTGGAGTGATGTTTTCACAAAACAGTTCGCCAGGGAGTATGCAAGCAGAAATA 898
Db 121 CCAAGGCTGGAGTGATGTTTTCACAAAACAGTTCGCCAGGGAGTATGCAAGCAGAAATA 180

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Qy 899 TCAATGTAATGCTATTGACACAGGTTTCAATGATCTGATGATGCTGCCGACTTGGAG 958
Db 181 TCAATGTAATGCTATTGACACAGGTTTCAATGATCTGATGATGCTGCCGACTTGGAG 240
Qy 959 AAGAGCTTGAGAGAAATCTTTGTCACCAATTCCTGTTAGGAGATATGCGCAACAGAGG 1018
Db 241 AAGAGCTTGAGAGAAATCTTTGTCACCAATTCCTGTTAGGAGATATGCGCAACAGAGG 300
Qy 1019 AAGTTGACGGGTTGCTGAGTTCTTGGCCCTTAACCCCGCAGCTAGCTATATGACTGGAC 1078
Db 301 AAGTTGACGGGTTGCTGAGTTCTTGGCCCTTAACCCCGCAGCTAGCTATATGACTGGAC 360
Qy 1079 AGGTGCTTACAAATGACGAGGGATGTAATGTAAGATTTGAGTTAGCTTGTGACACTTC 1138
Db 361 AGGTGCTTACAAATGACGAGGGATGTAATGTAAGATTTGAGTTAGCTTGTGACACTTC 420
Qy 1139 TACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTCACCGGGCGAATTTGGACAAC 1198
Db 421 TACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTCACCGGGCGAATTTGGACAAC 480
Qy 1199 AAATAGTTGTTCTCTTTCTTTGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1258
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Qy 1259 GAAGTTGAAA 1268
Db 541 GAAGTTGAAA 550

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DEFINITION BE510479.1 x1 946 - tassal primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION BE510479
VERSION BE510479.1 GI:9731727
KEYWORDS EST.
SOURCE Zea mays

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ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 600)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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/lab_host="XLOLR"
/clone_lib="946 - tassal primordium prepared by Schmidt
lab"
/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."

```

```

JOURNAL COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946053 row: B column: 11.
Location/Qualifiers
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/organism="Zea mays"
/mol_type="mRNA"
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inflorescence development"
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lab"
/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."

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source
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/organism="Zea mays"
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/tissue_type="tassels"
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inflorescence development"
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lab"
/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."

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BASE COUNT 172 a 148 c 105 g 175 t
ORIGIN
Query Match 41.4%; Score 549; DB 10; Length 600;
Best Local Similarity 99.8%; Pred. No. 1.6e-67;
Matches 599; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 653 ACACATTTGTTGATGAGGATGAAGAATCTCAGTGGCAAGACGTAATTAATGATCTGAATCTTAA 712
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Qy 713 CTGCGCTCTTCCCTTTGACACAGGCTCAACAAAGTAATCATCAAAAAGAGAAAGGAA 772
Db 540 CTGCGCTCTTCCCTTTGACACAGGCTCAACAAAGTAATCATCAAAAAGAGAAAGGAA 481
Qy 773 AAATATCAACATTTGATCTGTAGTTGCTTCTTCTGCAATTTGTTGGCAAGCTAATTAATA 832
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Db 300 TTGGAGAAGAGCTTTGAGAAGAAATCTTTGTCAACCATTCCTGTTAGGAGATATGCCCAAC 241
Qy 1013 CAGAGGAGTTGTCAGGCTTGGTTCAGTTCTTGGCCCTTAACCCCGCAGCTAGCTATATGA 1072
Db 240 CAGAGGAGTTGTCAGGCTTGGTTCAGTTCTTGGCCCTTAACCCCGCAGCTAGCTATATGA 181
Qy 1073 CTGGACAGGCTCTTACCAATTTGACGAGGAGTGGTAATGTAAGATTTGAGTTAGCTTGAATG 1132
Db 180 CTGGACAGGCTCTTACCAATTTGACGAGGAGTGGTAATGTAAGATTTGAGTTAGCTTGAATG 121
Qy 1133 CACTTCTACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTCACGGGCGAATTTTG 1192
Db 120 CACTTCTACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTCACGGGCGAATTTTG 61
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RESULT 6
BQ779235
LOCUS BQ779235 618 bp mRNA linear EST 26-JUL-2002
DEFINITION BQ779235.1 y1 946 - tassal primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION BQ779235
VERSION BQ779235.1 GI:21987707
KEYWORDS EST.
SOURCE Zea mays

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ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 618)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

```

```

JOURNAL COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

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FEATURES

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/clone_lib="946 - tassal primordium prepared by Schmidt lab"
/note="Organs: tassels; Vector: HybrizAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybrizAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
180 a 108 c 159 g 170 t 1 others

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Best Local Similarity 100.0%; Pred. No. 3.9e-59;

Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 718 GTCTTCTTTGTACACAGGCTGCAACAAAAGTAATCATGAAAAGAGAAAGGAGAAAAT 777

Db 74 GTCTTCTTTGTACACAGGCTGCAACAAAAGTAATCATGAAAAGAGAAAGGAGAAAAT 133

QY 778 ATCAACATTGCATCTAGTGTCTTACTGGCAATGTTGGCCAACTAATTATAGCGCA 837

Db 134 ATCAACATTGCATCTAGTGTCTTACTGGCAATGTTGGCCAACTAATTATAGCGCA 193

QY 838 GCCAAGCTGGAGTATGTTTCAAAAACAGTTGCCAGGAGTATCGACGAGAAAT 897

Db 194 GCCAAGCTGGAGTATGTTTCAAAAACAGTTGCCAGGAGTATCGACGAGAAAT 253

QY 898 ATCAATGTGAATGCTATTGCACAGGTTTCATTGCTATGATGATGCTCCGAACTTGA 957

Db 254 ATCAATGTGAATGCTATTGCACAGGTTTCATTGCTATGATGATGCTCCGAACTTGA 313

QY 958 GAAGAGCTTGAGAGAAATCTTGTCAACATTCGTTAGGAGATATGCGCAACAGAG 1017

Db 314 GAAGAGCTTGAGAGAAATCTTGTCAACATTCGTTAGGAGATATGCGCAACAGAG 373

QY 1018 GAAGTGCAGGTTGTCAGTCTCTGCGCCCTTAACCCGAGCTAGCTATATGACTGA 1077

Db 374 GAAGTGCAGGTTGTCAGTCTCTGCGCCCTTAACCCGAGCTAGCTATATGACTGA 433

QY 1078 CAGGTGCTTTACAAATTGACGGAGGATGTAATGTAAGATTTCAGTTAGCTTGCATGCACTT 1137

Db 434 CAGGTGCTTTACAAATTGACGGAGGATGTAATGTAAGATTTCAGTTAGCTTGCATGCACTT 493

QY 1138 CTACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTGACGGCGGATTTTGACAA 1197

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QY 1198 CAAATTAG 1205

Db 554 CAAATTAG 561

RESULT 7

CD484893/c

LOCUS

DEFINITION

3529_1_110_1_c12.x.1 3529 - 2 mm ear tissue from Schmidt and Hake

CD484893

ACCESSION

VERSION

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
Walbot.V.
Maize ESTs from various cDNA libraries sequenced at Stanford University
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3529_1_110_1 row: C column: 12.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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/db_xref="taxon:4577"
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/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake labs"
/note="Organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu amplified. Ampicillin is the selection marker."
183 a 169 c 116 g 191 t

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Best Local Similarity 100.0%; Pred. No. 8.6e-58;

Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 716 GCGTCTTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAAAAGAGAAAGGAAAAA 775

Db 511 GCGTCTTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAAAAGAGAAAGGAAAAA 452

QY 776 TTATCAACATTCGATCTGATGTTGCTTCTTACTGGCAATGTTGGCCAACTAATTATAGCG 835

Db 451 TTATCAACATTCGATCTGATGTTGCTTCTTACTGGCAATGTTGGCCAACTAATTATAGCG 392

QY 836 CAGCCAGGCTGGAGTGTGTTTTCACAAAACAGTTGCCAGGAGTATCGAAGCAGAA 895

Db 391 CAGCCAGGCTGGAGTGTGTTTTCACAAAACAGTTGCCAGGAGTATCGAAGCAGAA 332

QY 896 ATATCAATGTGAATGCTATTGCACAGGTTTCATTCATCTGATGATGATGATGATGATG 955

Db 331 ATATCAATGTGAATGCTATTGCACAGGTTTCATTCATCTGATGATGATGATGATGATG 272

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Db 271 GAGAAGAGCTTGAAGAAGAAATCTTGTCAACCATTCGTTAGGGAGATATGCGCAACACAG 212

QY 1016 AGGAAGTTCAGGCTTGGTTCGAGTTCTTGGCCCTTAACCCGAGCTAGCTATATGACTG 1075

Db 211 AGGAAGTTCAGGCTTGGTTCGAGTTCTTGGCCCTTAACCCGAGCTAGCTATATGACTG 152

QY 1076 GACAGGTGCTTACAAATTGACGAGGAGTGTGTAATGTAAGATTTGAGTTAGCTTATGTC 1133

Db 151 GACAGGTGCTTACAAATTGACGAGGAGTGTGTAATGTAAGATTTGAGTTAGCTTATGTC 94

RESULT 8

BO744718

LOCUS

DEFINITION

B0744718

639 bp mRNA linear EST 17-JUL-2002

tassel primordium prepared by Schmidt lab Zea

QY	640	GGGATTACAGACGACACATTGTTGATCAGGATGAAGAAATCTCAGTGGCAAGACGTAATT	699
Db	440	GGGATTACAGACGACACATTGTTGATCAGGATGAAGAAATCTCAGTGGCAAGACGTAATT	499
QY	700	GATCTGAATCTTACTTGGCGCTTCTCCITTTGTACACAGGCTGCACAAAGATGAATGATGAAA	759
Db	500	GATCTGAATCTTACTTGGTGTCCTTCTTTGTACACAGGCTGCACAAAGATGAATGATGAAA	559
QY	760	AGAGAAAGGGAATAATATCAACATTGCACTCTGTAGTTGGTCTTACTTGGCAATGTGGC	819
Db	560	AGAGAAAGGGAATAATATCAACATTGCACTCTGTAGTTGGTCTTACTTGGCAATGTGGC	619
QY	820	CAAGCTAATTATAGCGCAGC	839
Db	620	CAAGCTAATTATAGCGCAGC	639
RESULT 9			
LOCUS	CD510389	457 bp	linear
DEFINITION	3529_1110_1_C12.Y.1 3529 - 2 mm ear tissue from Schmidt and Hake		EST 05-JUN-2003
ACCESSION	CD510389	labs Zea mays cDNA, mRNA sequence.	
VERSION	CD510389.1	GI:31440958	
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	1 (bases 1 to 457)		
TITLE	Walbot,V.		
JOURNAL	Maize ESTs from various cDNA libraries sequenced at Stanford University		
COMMENT	Unpublished Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 3529 1,110 1 row: C column: 12.		
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	/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake labs"		
	/note="Organ: ear; Vector: PAD-GL4-2.1; Site 1: EcoRI; Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu amplified. Ampicillin is the selection marker."		
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Best Local Similarity	100.0%; Pred. No. 9.6e-55;		
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Db	61	TGCATCTCCAAAGCACATGCTCCCTCTTGGCTTCCGCTCTCTCTTGGGTCTCTTGGCGT	120

QY	640	GGGATTACAGACGACACATTGTTGATCAGGATGAAGAAATCTCAGTGGCAAGACGTAATT	699
Db	440	GGGATTACAGACGACACATTGTTGATCAGGATGAAGAAATCTCAGTGGCAAGACGTAATT	499
QY	700	GATCTGAATCTTACTTGGCGCTTCTCCITTTGTACACAGGCTGCACAAAGATGAATGATGAAA	759
Db	500	GATCTGAATCTTACTTGGTGTCCTTCTTTGTACACAGGCTGCACAAAGATGAATGATGAAA	559
QY	760	AGAGAAAGGGAAGAAATATCAACATTGCACTCTGTAGTTGGTCTTACTGGCAATGTGGC	819
Db	560	AGAGAAAGGGAAGAAATATCAACATTGCACTCTGTAGTTGGTCTTACTGGCAATGTGGC	619
QY	820	CAAGCTAATTATAGCGCAGC	839
Db	620	CAAGCTAATTATAGCGCAGC	639
RESULT 9			
LOCUS	CD510389	457 bp	linear
DEFINITION	3529_1110_1_C12.Y.1 3529 - 2 mm ear tissue from Schmidt and Hake		EST 05-JUN-2003
ACCESSION	CD510389	labs Zea mays cDNA, mRNA sequence.	
VERSION	CD510389.1	GI:31440958	
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	1 (bases 1 to 457)		
TITLE	Walbot,V.		
JOURNAL	Maize ESTs from various cDNA libraries sequenced at Stanford University		
COMMENT	Unpublished Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 3529 1,110 1 row: C column: 12.		
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	/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake labs"		
	/note="Organ: ear; Vector: PAD-GL4-2.1; Site 1: EcoRI; Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu amplified. Ampicillin is the selection marker."		
BASE COUNT	73 a 164 c 122 g		
ORIGIN			
Query Match	34.5%; Score 457; DB 14; Length 457;		
Best Local Similarity	100.0%; Pred. No. 9.6e-55;		
Matches 457; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	23	GTCCCCCAATAGACTCTCCCATCCGTCGTCTGTCTCCGTCACGGCTCAAACTACTCCGCC	82
Db	1	GTCCCCCAATAGACTCTCTCCCATCCGTCGTCTGTCTCCGTCACGGCTCAAACTACTCCGCC	60
QY	83	TGCATCTCCAAAGCACATGCTCCCTCTGGCTTCCGCTCTCTCTTTCGGCTCTCTTCGCGT	142
Db	61	TGCATCTCCAAAGCACATGCTCCCTCTGGCTTCCGCTCTCTCTTTCGGCTCTCTTCGCGT	120

143 CCCGAGCCCTCATGCGCCAGCCGCGCCACCGCAGCAGCAGCAGCTCTCTCC 202
 121 CCCGAGCCCTCATGCGCCAGCCGCGCCACCGCAGCAGCAGCAGCTCTCTCC 180
 203 CGGCTGCGCGTGGAGCAGCCGCGCGCGCGCGCTCCCGCGGGGTTCTGTCAGTTTG 262
 181 CGGCTGCGCGTGGAGCAGCCGCGCGCGCGCGCTCCCGCGGGGTTCTGTCAGTTTG 240
 263 GTGAGGCGCGCGCGCTCTCTCCAGCTGCGGTCCGCGCGGGTCTCTGCTGTCGTCGTC 322
 241 GTGAGGCGCGCGCGCTCTCTCCAGCTGCGGTCCGCGCGGGTCTCTGCTGTCGTCGTC 300
 323 AAACCCATGTTGCTGCTGTAACAGCAGTGTAAAGATGCTACCAAGCTGGAAGCTC 382
 301 AAACCCATGTTGCTGCTGTAACAGCAGTGTAAAGATGCTACCAAGCTGGAAGCTC 360
 383 CAGTTGTTGTTGTTACAGTGCATCTAGAGGATGTTAAGCAACTCTCTAGCCCTTG 442
 361 CAGTTGTTGTTGTTACAGTGCATCTAGAGGATGTTAAGCAACTCTCTAGCCCTTG 420
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 421 GAAAGCAGGATGCAAGCTTCTGTTAAACTATGCCCG 457

RESULT 10
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 LOCUS 946157G10.y1 946 - tassal primordium prepared by Schmidt lab Zea
 DEFINITION mays cDNA, mRNA sequence.

ACCESSION BU092794
 VERSION BU092794.1 GI:22542341
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 539)
 Walbot,V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946157 row: G column: 10.
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 /cultivar="OH43"
 /db_xref="taxon:4577"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to
 inflorescence development"
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 /clone_lib="946 - tassal primordium prepared by Schmidt
 lab"
 /note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
 Site 2: XhoI; George Chuck dissected immature tassels
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybriZAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."

BASE COUNT 157 a 94 c 141 g 146 t 1 others
 ORIGIN
 Query Match 34.0%; Score 451; DB 13; Length 539;
 Best Local Similarity 99.8%; Pred. No. 5.5e-54;

Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 4 TGTGTAGAGATGAAGAAATCTCAGTGGCAAGACGTAATTGATCTGAATCTTACTGCG 63
 QY 719 TCTTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAAAAAGAGAAAGGAAAAATTA 778
 Db 64 TCTTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAAAAAGAGAAAGGAAAAATTA 123
 QY 779 TCACATTCATCTGTAGTTGGTCTTACTGCAATGTTGCCAAGCTTAATTATAGCCAG 838
 Db 124 TCACATTCATCTGTAGTTGGTCTTACTGCAATGTTGCCAAGCTTAATTATAGCCAG 183
 QY 839 CCAGGCTGCAAGTGAATGTTTCAAAAAACAGTTGCCAGGAGTATGCAAGCAGAATA 898
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 Db 244 TCAATGTGAATGCTATTGCAACAGGCTTCATGATCTGATATGACTGCCGAACTTGGAG 303
 QY 959 AAGAGCTTGAGAAAGAAATCTTGTCAACCATTCGGTTAGGAGATATGCGCCACACAGG 1018
 Db 304 AAGAGCTTGAGAAAGAAATCTTGTCAACCATTCGGTTAGGAGATATGCGCCACACAGG 363
 QY 1019 AAGTTCAGGTTGGTGGAGTCTCTGCGCCCTTAACCCCGCAGCTAGCTATATGACTGGAC 1078
 Db 364 AAGTTCAGGTTGGTGGAGTCTCTGCGCCCTTAACCCCGCAGCTAGCTATATGACTGGAC 423
 QY 1079 AGTGCTTACAATGACGAGGAGTGTATGTAAGATTGAGTTGAGTTGAGTTCGACCTTC 1138
 Db 424 AGTGCTTACAATGACGAGGAGTGTATGTAAGATTGAGTTGAGTTGAGTTCGACCTTC 483
 QY 1139 TACTTTGCTGAGCAATTAATG 1160
 Db 484 TACTTTGCTGAGCAATTAATG 505

RESULT 11
 BO667989

LOCUS 946102B05.y1 946 - tassal primordium prepared by Schmidt lab Zea
 DEFINITION mays cDNA, mRNA sequence.

ACCESSION BO667989
 VERSION BO667989.1 GI:21809671
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 530)
 Walbot,V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946102 row: E column: 05.
 Location/Qualifiers
 1. 530
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 /cultivar="OH43"
 /db_xref="taxon:4577"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to

REFERENCE 1

AUTHORS Walbot V
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL Unpublished
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
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 Plate: 946102 row: E column: 05.
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 /dev_stage="just after the transition from vegetative to

FEATURES
 source
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 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="OH43"
 /db_xref="taxon:4577"
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 /dev_stage="just after the transition from vegetative to

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/notes="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
Site_2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."
154 a 95 c 132 g 147 t 2 others
BASE COUNT
ORIGIN

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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 648)
 Walbot, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL
COMMENT

Unpublished

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946134 row: D column: 10.

FEATURES
source

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/lab_host="XLOLR"
/clone_lib="946 - tassels primordium prepared by Schmidt lab"
/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
164 a 159 c 184 g 141 t

Query Match 30.0%; Score 398; DB 13; Length 648;
Best Local Similarity 99.5%; Pred. No. 9e-47;
Matches 548; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 220 GCCGGGGCGCGCGCGCTCCCGCGGGGTTCTGTCAGTTTGGTGGAGGCGCGCGCGC 279
DB 83 GCCGGGGCGCGCGCGCTCCCGCGGGGTTCTGTCAGTTTGGTGGAGGCGCGCGC 142
QY 280 TTCTCTCCAGCTCGCTCGCGCGGTTCTGTTGTCAGTTCGAAACCATGTTGCTGCT 339
DB 143 TTCTCTCCAGCTCGCTCGCGCGGTTCTGTTGTCAGTTCGAAACCATGTTGCTGCT 202
QY 340 GTTGAACAAGCAGTTGTTAAAGATCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 399
DB 203 GTTGAACAAGCAATTGTTAAAGATCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 262
QY 400 GGTGATCTAGAGGATTGTTAAGCACTGCTAGCCCTTGAAGAGCAGGATGCAAG 459
DB 263 GGTGATCTAGAGGATTGTTAAGCACTGCTAGCCCTTGAAGAGCAGGATGCAAG 322
QY 460 GTTCTGTAAACTATGCGCGGTCCTCGAAAGAGGCTGAAGAGGCTCCAAAGAGATTGAA 519
DB 323 GTTCTGTAAACTATGCGCGGTCCTCGAAAGAGGCTGAAGAGGCTCCAAAGAGATTGAA 382
QY 520 GCATCTGTGTGAGGCTATCACTTTCGAGAGAGATGTTCAAAGAGCTGATGATGAG 579
DB 383 GCATCTGTGTGAGGCTATCACTTTCGAGAGAGATGTTCAAAGAGCTGATGATGAG 442
QY 580 TCTATGATGAAGCAGCTCTAGATAAATGGGGAACAATAGATGCTGTTAAATAATGCA 639
DB 443 TCTATGATGAAGCAGCTCTAGATAAATGGGGAACAATAGATGCTGTTAAATAATGCA 502
QY 640 GGGATTACACGAGACATGTTGATGAGGATGAAGAAATCTCATGTGCGAAGAGTAAT 699
DB 503 GGGATTACACGAGACATGTTGATGAGGATGAAGAAATCTCATGTGCGAAGAGTAAT 562
QY 700 GATCTGAATCTTACGGGCTTCTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAA 759
DB 563 GATCTGAATCTTACGGGCTTCTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAA 622
QY 760 AAGAGAAAGG 770
DB 623 AAGAGAAAGG 633

RESULT 14
BM737475/cLOCUS
DEFINITION

952056D06.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 952056 row: D column: 06.

Location/Qualifiers

1. .589

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="BMS (Black Mexican Sweet)"

/db_xref="taxon:4577"

/tissue_type="suspension culture"

/dev_stage="mixed logarithmic and stationary growth phases"

/lab_host="DH10B"

/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"

/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Length

Score

Pred. No.

2.6e-46;

29.8%;

Score 395;

DB 12;

Length 589;

0; Mismatches

2; Indels

0; Gaps

0;

QY 220

GCCGGGGCGCGCGCGCTCCCGCGGGGTTCTGTCAGTTTGGTGGAGGCGCGCGC 279

DB 540

GCCGGGGCGCGCGCGCTCCCGCGGGGTTCTGTCAGTTTGGTGGAGGCGCGCGC 481

QY 280

TTCTCTCCAGCTCGCTCGCGCGGTTCTGTTGTCAGTTCGAAACCATGTTGCTGCT 339

DB 480

TTCTCTCCAGCTCGCTCGCGCGGTTCTGTTGTCAGTTCGAAACCATGTTGCTGCT 421

QY 340

GTTGAACAAGCAGTTGTTAAAGATCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 399

DB 420

GTTGAACAAGCAATTGTTAAAGATCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 361

QY 400

GGTGCATCTAGAGGATTGTTAGGCAACTGCTCTAGCCCTTGAAGAGCAGGATGCAAG 459

DB 360

GGTGCATCTAGAGGATTGTTAGGCAACTGCTCTAGCCCTTGAAGAGCAGGATGCAAG 301

QY 460

GTTCTGTAAACTATGCGCGGTTCTCGAAAGAGGCTGAAGAGGCTTCCCAAGAGATTGAA 519

Db 300 GTTCTGGTAAACTATGCGCGTCTCGAAGAGGCTGAGAGGTCTCCAAAGAGATTGAA 241
 Qy 520 GCATCTGGTGGTGGAGGCTATACCTTCGAGAGAGATGTTTCAAAGAGAGCTGATGAGAG 579
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 Qy 580 TCTATGATGAAGAGAGCTTATAGATAAATGGGAAACAATAGATGCTGCTGTAATAATGCA 639
 Db 180 TCTATGATGAAGAGAGCTTATAGATAAATGGGAAACAATAGATGCTGCTGTAATAATGCA 121
 Qy 640 GGGATTACACGAGACACATGTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAATT 699
 Db 120 GGGATTACACGAGACACATGTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAATT 61
 Qy 700 GATCTGAATCTTACTGG 716
 Db 60 GATCTGAATCTTACTGG 44

RESULT 15
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 LOCUS
 DEFINITION BE510480 626 bp mRNA linear EST 07-AUG-2000
 946053B11.y1 946 - tassels primordium prepared by Schmidt lab Zea
 mays cDNA, mRNA sequence.
 ACCESSION BE510480
 VERSION BE510480.1 GI:9731728
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 626)

REFERENCE Walbot, V.
 AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford
 TITLE University

JOURNAL Unpublished
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946053 row: B Column: 11.
 Location/Qualifiers

FEATURES
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 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="OH43"
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 /dev_stages="just after the transition from vegetative to
 inflorescence development"
 /lab_host="XLOLR"
 /clone_lib="946 - tassels primordium prepared by Schmidt
 lab"
 /note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
 Site 2: XhoI; George Chuck dissected immature tassels
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybriZAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."
 BASE COUNT 136 a 169 c 175 g 146 t
 ORIGIN

Query Match 29.8%; Score 395; DB 10; Length 626;
 Best Local Similarity 99.6%; Pred. No. 2.4e-46;
 Matches 495; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 220 GCCGGGGCGCGCGCGTCCCGGGGGTTCGTCACGTTTGGTGGAGGCGCGCGCGC 279
 Db 114 GCCGGGGCGCGCGCGTCCCGGGGGTTCGTCACGTTTGGTGGAGGCGCGCGCGC 173

Search completed: November 7, 2003, 19:33:22
 Job time : 3157 secs

Qy 280 TTCTCTCCACGCTGCGGTCCGGCGGTTCCTCTGCTGTGCAAAACCCATGTTCTGCT 339
 Db 174 TTCTCTCCACGCTGCGGTCCGGCGGTTCCTCTGCTGTGCAAAACCCATGTTCTGCT 233
 Qy 340 GTTGAACAAGCAGATTGTAAGAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 399
 Db 234 GTTGAACAAGCAGATTGTAAGAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 293
 Qy 400 GGTGCATCTAGAGGAGATTGGTAAGCAACTGCTCTAGCCCTTGGAAAAAGCAGGATGCAAG 459
 Db 294 GGTGCATCTAGAGGAGATTGGTAAGCAACTGCTCTAGCCCTTGGAAAAAGCAGGATGCAAG 353
 Qy 460 GTTCTGGTAAACTATGCCCGGTCTCTCGAAAAGAGGCTGAAGAGTCTCAAAGAGATTGAA 519
 Db 354 GTTCTGGTAAACTATGCCCGGTCTCTCGAAAAGAGGCTGAAGAGTCTCAAAGAGATTGAA 413
 Qy 520 GCATCTGGTGTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAGAGAGCTGATGTAGAG 579
 Db 414 GCATCTGGTGTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAGAGAGCTGATGTAGAG 473
 Qy 580 TCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGCTGCTGTAATAATGCA 639
 Db 474 TCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGCTGCTGTAATAATGCA 533
 Qy 640 GGGATTACACGAGACACATTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAATT 699
 Db 534 GGGATTACACGAGACACATTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAATT 593
 Qy 700 GATCTGAATCTTACTGG 716
 Db 594 GATCTGAATCTTACTGG 610